

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2002, 10:12:27 ; Search time 29.49 Seconds
(without alignments)
741.999 Million cell updates/sec

Title: US-09-299-139A-1
Perfect score: 197
Sequence: 1 SQPQVPPYASQNRDQE.....QSDTTCNKPLPLPPMSGT 197

Scoring table:
Gap 60.0 , Gapext 60.0
Searched: 747574 seqs, 111073796 residues
Word size : 0
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1980.DAT.*
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3: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1982.DAT.*
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21: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	197	100.0	197	AAW23220	Extracellular doma
2	197	100.0	197	AAW23220	Human lymphotoxin
3	77	39.1	77	AAW94642	TNF-R extracellula
4	77	39.1	77	AAW69194	Human TNF-R extrac
5	19	9.6	38	AAW04498	TNFR molecule LT-b
6	10	5.1	415	AAW36700	Human tumour necro
7	7	3.6	71	AAW20502	Human neurofilamen
8	7	3.6	75	AAW65981	Propionibacterium
9	7	3.6	80	AAW20744	Novel human diagra
10	7	3.6	94	AAW58231	Propionibacterium
11	7	3.6	104	ABG08131	Novel human diagra

12	7	3.6	109	22	AAU50142	Propionibacterium
13	7	3.6	129	22	ABG01762	Novel human diagra
14	7	3.6	178	22	ABG05157	Novel human diagra
15	7	3.6	211	21	ABG05558	Arabidopsis thalia
16	7	3.6	231	21	ABG01763	Novel human diagra
17	7	3.6	252	21	ABG15889	Arabidopsis thalia
18	7	3.6	260	21	ABG55557	Arabidopsis thalia
19	7	3.6	274	21	ABG55556	Arabidopsis thalia
20	7	3.6	277	21	ABG15888	Arabidopsis thalia
21	7	3.6	290	21	ABG15887	Arabidopsis thalia
22	7	3.6	437	16	AAW76521	Alpha-amylase-8-C
23	7	3.6	437	21	AAW12799	Rice alpha-Amy8-C
24	7	3.6	437	22	AAW50252	Rice alpha-amylase
25	7	3.6	437	22	ABG97246	Alpha-amylase rela
26	7	3.6	493	22	ABG91139	C glutamicum prote
27	7	3.6	559	20	AAW05657	Maize 4-coumarate;
28	7	3.6	689	22	AAW01020	Human pif-1 type h
29	7	3.6	760	22	ABW62427	Drosophila melanog
30	7	3.6	1111	22	AAW37362	Staphylococcus aur
31	7	3.6	2000	22	AAW61853	Myxoma virus immun
32	7	3.6	2392	21	AAW07665	Amino acid sequenc
33	6	3.0	8	16	AAW79485	Primer generating
34	6	3.0	10	22	AAW97202	Human complementar
35	6	3.0	12	21	AAW93840	Reactive peptide w
36	6	3.0	13	13	AAW28478	Sequence of synthe
37	6	3.0	14	13	AAW28479	Sequence of synthe
38	6	3.0	15	13	AAW28480	Sequence of synthe
39	6	3.0	16	13	AAW28481	Sequence of synthe
40	6	3.0	17	13	AAW28482	Sequence of synthe
41	6	3.0	18	13	AAW28483	Sequence of synthe
42	6	3.0	19	18	AAW41620	Peptide used in pr
43	6	3.0	19	22	AAW66972	OPG peptide fragme
44	6	3.0	22	9	AAW81130	c-rat-related pept
45	6	3.0	23	13	AAW25941	N-terminal peptide

ALIGNMENTS

RESULT 1
AAW23220
ID AAW23220 standard; protein; 197 AA.
XX AC AAW23220;
XX DT 29-OCT-1997 (first entry)
XX DE Extracellular domain of human lymphotoxin beta receptor.
XX Human; lymphotoxin beta; receptor; blocking agent; extracellular;
XX ligand binding; domain; treatment; Th1 cell; immune response;
XX delayed; hypersensitivity; contact; tuberculin; granulomatous;
XX graft versus host; disease; organ rejection; autoimmune; disorder;
XX multiple sclerosis; insulin dependent diabetes; uveitis; cytokine;
XX Mycobacterium; abnormal; lymphoid organ; development.
XX Homo sapiens.
XX OS WO9703687-A1.
XX PD 06-FEB-1997.
XX PF 19-JUL-1996; 96WO-US12010.
XX PR 21-JUL-1995; 95US-0505606.
XX PA (BIOJ) BIOGEN INC.
XX PI Benjamin CD, Browning JL, Hochman PS;
XX DR WPI; 1997-132373/12.
XX

PT Compositions comprising lymphotoxin-beta receptor blocking agent
 PT used to treat auto-immune diseases, e.g. sclerosis,
 PT insulin-dependent diabetes, etc.

XX Example 1; Pages 55-56; 76pp; English.

XX The present sequence, a human lymphotoxin beta receptor (LT-beta-R)
 CC blocking agent, comprises the extracellular ligand binding domain
 CC of the human LT-beta-R up to the transmembrane region. It can be
 CC used to treat a Th1 cell mediated immune response which contributes
 CC to a delayed type hypersensitivity reaction, preferably contact,
 CC tuberculin type or granulomatous hypersensitivity, graft versus
 CC host disease, organ rejection or an autoimmune disorder, i.e.
 CC multiple sclerosis, insulin dependent diabetes, sympathetic
 CC ophthalmia, uveitis and psoriasis. It can also be used to treat
 CC conditions exacerbated by the activities of Th-1 type cytokines, or
 CC Listeria, Toxoplasma or Mycobacterium infection. Its ability to
 CC selectively or partially block the LT-beta-R pathway may be useful
 CC in the treatment of abnormal lymphoid organ development associated
 CC with misexpression or overexpression of signalling by the LT-beta-R
 CC pathway. The present LT-beta-R blocking agent is capable of
 CC selectively inhibiting Th1, but not Th2 cell dependent immune
 CC effector mechanisms. As Th1 cytokines can inhibit Th2 cell
 CC dependent responses, the present LT-beta-R blocking agent may also
 CC indirectly stimulate certain Th2 cell dependent responses which are
 CC normally inhibited by Th1 induced cytokines. Doses of about 1 mg/kg
 CC of the present soluble LT-beta-R are expected to be suitable
 CC starting doses for optimising treatment.

XX Sequence 197 AA;

Query Match 100.0%; Score 197; DB 18; Length 197;
 Best Local Similarity 100.0%; Pred. No. 4.2e-200;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASNQTCRDOEKEYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 60
 Db 1 sqpavppyasentqcrdqeqeyepqhricsrcppgttyvsaksrirdtvcataens 60
 QY 61 YNEHWNLTICQLCRPCDPVMGLEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 Db 61 ynehwnlyticqlcrpcdpvmgleiapctskrktqcrqcpgmfcawalecthcellsd 120
 QY 121 CPPGTEAEELKDEVGKGNHCVPCRKAGHFQNTSSPSARCPHTRCENQGLVEAPGTAQSD 180
 Db 121 cpggteaelkdevgkgnhcvpcrkaghfqntsspsarcphtrcencglveeapgtagsd 180
 QY 181 TTCKNPLEPLPPMSGT 197
 Db 181 ttcknpleplppmsgt 197

RESULT 2

ID AAY31326 standard; peptide; 197 AA.

XX AAY31326;

XX 04-OCT-1999 (first entry)

DE Human lymphotoxin (LT)beta-receptor extracellular region.

XX Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;
 KW immune system; tumour; follicular lymphoma; extracellular domain; human.

XX Homo sapiens.

XX WO9938525-A1.

XX 05-AUG-1999.

XX 29-JAN-1999; 99WO-US01928.

XX 02-FEB-1998; 98US-0073410.
 PR 30-JAN-1998; 98US-0073112.

XX (BIOJ) BIOGEN INC.

XX Browning J, Thorbecke J, Tsiagbe V;

XX WPI; 1999-469242/39.

XX New method of treating follicular lymphomas by inhibiting
 PT interaction between lymphotoxin-beta and its receptor

XX Example 1; Page 25-26; 31pp; English.

XX The invention provides a method for arresting or reducing severity of
 CC effects of a tumour by administration of a composition which inhibits
 CC the interaction between lymphotoxin (LT)-beta and its receptor. An
 CC inhibitor of the interaction between LT-beta and its receptor can be
 CC administered for altering the survival or maintenance of follicular
 CC dendritic cells in a subject and for altering the architecture of the
 CC organs of the immune system. The method is useful for treating tumours,
 CC specifically follicular lymphomas. It offers an alternative therapy for
 CC those with tumours resistant to traditional chemotherapy. The present
 CC sequence represents the extracellular region of the human LTbeta-receptor
 CC and comprises the ligand binding domain.

XX Sequence 197 AA;

Query Match 100.0%; Score 197; DB 20; Length 197;
 Best Local Similarity 100.0%; Pred. No. 4.2e-200;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASNQTCRDOEKEYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 60
 Db 1 sqpavppyasentqcrdqeqeyepqhricsrcppgttyvsaksrirdtvcataens 60
 QY 61 YNEHWNLTICQLCRPCDPVMGLEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 Db 61 ynehwnlyticqlcrpcdpvmgleiapctskrktqcrqcpgmfcawalecthcellsd 120
 QY 121 CPPGTEAEELKDEVGKGNHCVPCRKAGHFQNTSSPSARCPHTRCENQGLVEAPGTAQSD 180
 Db 121 cpggteaelkdevgkgnhcvpcrkaghfqntsspsarcphtrcencglveeapgtagsd 180
 QY 181 TTCKNPLEPLPPMSGT 197
 Db 181 ttcknpleplppmsgt 197

RESULT 3

ID AAW94642 standard; peptide; 77 AA.

XX AAW94642;

XX 29-APR-1999 (first entry)

XX TNF-R extracellular Cys-rich domain TNF-R-IP.

XX Tumour necrosis factor receptor; TNF-R; autoimmune diseases;
 KW inflammation; septic shock; cachexia; graft versus host disease;
 KW skin allergic reaction; immune complex disease; malaria;
 KW transplantation rejection.

XX Homo sapiens.

XX WO9853842-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-US10891.

FT	Misc-difference	/label= unknown
FT	Misc-difference 10	/label= unknown
FT	Misc-difference 19	/label= unknown
XX	WO200158953-A2.	
XX	16-AUG-2001.	
XX	09-FEB-2001; 2001WO-US04125.	
XX	11-FEB-2000; 2000US-O181909.	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
Pt	Lenardo MJ, Chan FK, Slegel RM;	
DR	WPI; 2001-502707/75.	
XX	A polypeptide comprising the isolated amino acid sequence of a	
Pt	pre-ligand assembly domain (PLAD) of a TNF-like receptor for inhibiting	
Pt	TNF receptor or Fas oligomerisation in a cell and for treatment of	
Pt	autoimmune disease -	
PS	Disclosure; Fig 3; 77pp; English.	
CC	The sequence represents a cysteine-rich domain (CRD1) of the tumour	
CC	necrosis factor receptor (TNFR) protein LT-beta-R, which comprises a	
CC	pre ligand assembly domain (PLAD). This protein and others of the TNFR	
CC	superfamily can be utilised to inhibit PLAD self-association, TNF	
CC	receptor or Fas oligomerisation in a cell and ligand binding to members	
CC	of the TNFR superfamily or Fas. The PLAD containing proteins are also	
CC	useful for treating inflammation associated with autoimmune disease and	
CC	in screening for inhibitors of PLAD association. The treatable disorders	
CC	include periodic fever syndromes, sepsis syndromes, adult respiratory	
CC	distress syndrome, ulcerative colitis, Crohn's disease, rheumatoid	
CC	arthritis, autoimmune gastritis, psoriasis, Still's disease, Behcet's	
CC	disease, Sjogren's syndrome, ankylosing spondylitis, autoimmune uveitis,	
CC	autoimmune lymphoproliferative syndrome (ALPS), hyper IgM syndrome,	
CC	multiple sclerosis, pernicious anaemia, Goodpasture's syndrome,	
CC	autoimmune orchitis, myasthenia gravis, polyendocrinopathies, diabetes	
CC	mellitus and thyroiditis.	
SO	Sequence 38 AA:	
Query Match	9.6%; Score 19; DB 22; Length 38;	
Best Local Similarity	100.0%; Pred. No. 1,9e-12;	
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY 35 CPPGTYSAKCSRIDRYVC 53		
iiiiiiiii		
Ddb 20 CPPGTYSAKCSRIDTVC 38		
RESULT# 6		
AAB36700		
ID AAB36700 standard; Protein; 415 AA.		
XX AAB36700;		
AC		
XX		
DT 15-MAR-2001 (first entry)		
DE Human tumour necrosis factor receptor LTRB protein SEQ ID NO:6.		
XX Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; noctropic;		
KW TRAIL receptor without intracellular domain; diagnostic; cytostatic;		
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;		
KW immunosuppressive; neuroprotective; antiviral; anti-inflammatory;		
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;		
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;		
KW apoptotic cell death related disease; autoimmune disorder;		

XX 30-MAY-1997; 97US-0866545.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX PI Greene ML, Murali R, Takasaki W;
 XX WPI: 1999-080781/07.
 XX
 XX New compounds designed from a binding loop of a tumour necrosis
 XX factor receptor - are capable of inhibiting the biological
 XX activities of tumour necrosis factor, e.g., in treating inflammation
 XX or autoimmune diseases
 XX
 XX Disclosure: Fig 1; 78pp; English.
 XX
 XX The present invention describes peptides and peptide analogues which
 XX correspond in primary sequence to a binding loop of a tumour necrosis
 XX factor receptor (TNF-R) superfamily member. The compounds are especially
 XX designed from a binding loop of TNF-R p55. They are capable of
 XX inhibiting TNF binding to its cellular receptors and may be used to
 XX inhibit the biological activities of TNF. They may be used in treating
 XX TNF-associated conditions such as acute and chronic inflammatory
 XX responses, septic shock, cachexia, autoimmunity, graft-versus-host
 XX disease, skin allergic reactions, immune complex disease,
 XX transplantation rejection and malaria. Administration is, e.g. oral,
 XX transdermal, transmucosal, pulmonary, subcutaneous, intravenous or
 XX intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present
 XX sequence represents an extracellular Cys-rich domain of TNF-R from the
 XX present invention.
 XX
 XX Sequence 77 AA:

Query Match 39.1%; Score 77; DB 20; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.6e-73;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNEHNNYLTICOLRCPCDPVMGLEETAPCTSKRKTCRCOPMFCANALE 111
 Db 1 vcatcaensynehnnylticqlcrpcdpvmgleetapctskrktcrcqpmfcaavale 60
 QY 112 CTNCELSDCPPTGEAE 128
 Db 61 ctncellsdcpptgeae 77

RESULT 4

AAB65194
 ID AAB69194 standard; protein: 77 AA.

XX
 AC AAB69194;

XX 30-APR-2001 (first entry)

XX Human TNF-R extracellular Cys-rich domain TNF-R- α SEQ ID NO:3.

XX Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
 XX osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic;
 XX antiinflammatory; antirheumatic; antinflammatory; immunomodulatory;
 XX tumour necrosis factor-related activation-induced cytokine; TRANCE;
 XX receptor activator of NF-kappaB ligand; RANK; osteoporosis;
 XX Paget's disease; metastatic bone disease; rheumatoid arthritis;
 XX periodontal disease; modulating dendritic cell maturation;
 XX T cell proliferation; CD40 receptor system.

XX Homo sapiens.

XX MO200108699-A1.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-US20510.

XX 28-JUL-1999; 99US-0146090.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX (AOKI/) AOKI K.
 XX (HORN/) HORNE W C.
 XX (BARO/) BARON R.
 XX
 XX Aoki K, Horne WC, Baron R, Greene ML, Murali R;
 XX WPI: 2001-182866/18.
 XX
 XX Use of peptides and peptide analogs which are TRANCE/RANK inhibitors,
 XX for inhibiting osteoclastogenesis and bone resorption
 XX
 XX Disclosure: Fig 1; 81pp; English.
 XX
 XX The present invention describes a method for inhibiting
 XX osteoclastogenesis and bone resorption. Osteoclastogenesis and bone
 XX resorption inhibiting peptide analogues from the present invention have
 XX osteopathic, cytostatic, antirheumatic, antinflammatory, antinflammatory
 XX and immunomodulatory activities, and are tumour necrosis factor (TNF)-
 XX related activation-induced cytokine (TRANCE)/receptor activator of
 XX NF-kappaB ligand (RANK) inhibitors. The method is useful for treating
 XX diseases characterised by bone loss such as osteoporosis, Paget's
 XX disease, metastatic bone disease, rheumatoid arthritis or periodontal
 XX disease, and modulating dendritic cell maturation, T cell proliferation,
 XX and/or CD40 receptor systems. The present sequence represents an
 XX extracellular Cys-rich domain of a tumour necrosis factor receptor
 XX (TNF-R) superfamily member, which is used in the exemplification of
 XX the present invention.
 XX
 XX Sequence 77 AA:

Query Match 39.1%; Score 77; DB 22; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.6e-73;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNEHNNYLTICOLRCPCDPVMGLEETAPCTSKRKTCRCOPMFCANALE 111
 Db 1 vcatcaensynehnnylticqlcrpcdpvmgleetapctskrktcrcqpmfcaavale 60
 QY 112 CTNCELSDCPPTGEAE 128
 Db 61 ctncellsdcpptgeae 77

RESULT 5

AAU04498
 ID AAU04498 standard; Peptide: 38 AA.

XX
 AC AAU04498;

XX 24-OCT-2001 (first entry)

XX TNFR molecule LR-beta-R cysteine-rich domain #1 (CRD1).

XX TNFR superfamily; tumour necrosis factor receptor superfamily; PLAD; Fas;
 XX pre-ligand assembly domain; oligomerisation; inflammation; psoriasis;
 XX periodic fever syndrome; sepsis syndrome; ulcerative colitis; ALPS;
 XX adult respiratory distress syndrome; rheumatoid arthritis; LR-beta-R;
 XX Crohn's disease; autoimmune gastritis; Still's disease; Behcet's disease;
 XX Sjogren's syndrome; ankylosing spondylitis; autoimmune uveitis;
 XX autoimmune lymphoproliferative syndrome; hyper IgM syndrome;
 XX multiple sclerosis; pernicious anaemia; Goodpasture's syndrome;
 XX autoimmune orchitis; myasthenia gravis; polyendocrinopathy; thyroiditis;
 XX diabetes mellitus.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 3

KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
PN WO9845322-A2.
XX
XX 15-OCT-1998.
XX
XX 02-APR-1998; 98WO-IB00705.
XX
XX 10-APR-1997; 97US-0043163.
XX
XX (UYUT-) RIJKSUNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX WPI; 1998-609901/51.
DR N-PSDB; AAX75758.
XX
XX Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also
PT for treatment and prevention with specific ribozymes or wild-type
PT RNA
XX
XX Disclosure; Figure 7; 258pp; English.
XX
XX This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC use of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A.
XX
XX Sequence 71 AA;
SQ

Query Match 3.6%; Score 7; DB 19; Length 71;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 151 TSSPSAR 157
| | | | |
Db 6 tsspsar 12
RESULT 8
ID AAU65981
XX AAU65981 standard; Protein; 75 AA.
XX
AC AAU65981;
XX
DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #26877.
DE
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US12865.
XX
XX 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
PI N-PSDB; AAS59704.
XX
XX WPI; 2001-616774/71.
DR
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris
XX
XX Example 1; SEQ ID No 27176; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 75 AA;
SQ

Query Match 3.6%; Score 7; DB 22; Length 75;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 151 TSSPSAR 157
| | | | |
Db 63 tsspsar 69
RESULT 9
ID ABG20744
XX ABG20744 standard; Protein; 80 AA.
XX
AC ABG20744;
XX

DT 18-FEB-2002 (first entry)
 XX Novel human diagnostic protein #20735.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS
 PN WO200175067-A2.
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR N-PSDB; AAS84931.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 51103; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 80 AA;
 Query Match 3.6%; Score 7; DB 22; Length 80;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 OGLVEAA 173
 Db 63 qglveaa 69
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 RESULT 10
 ID AAU58231 standard; Protein; 94 AA.
 XX AAU58231;
 AC
 XX 27-FEB-2002 (first entry)
 DT

XX Propionibacterium acnes immunogenic protein #19127.
 DE
 XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX 01-NOV-2001.
 PD
 XX 20-APR-2001; 2001WO-US12865.
 PF
 XX 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 XX 07-JUL-2000; 2000US-216747P.
 PR
 XX (CORI-) CORIXA CORP.
 PA
 XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59589.
 XX
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID No 19426; 1069pp; English.
 XX
 CC Sequences AU39105-AU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 94 AA;
 Query Match 3.6%; Score 7; DB 22; Length 94;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 151 TSSPSAR 157
 Db 82 tsspsar 88
 |||||
 RESULT 11
 ID ABG08131 standard; Protein; 104 AA.
 XX ABG08131;
 AC
 XX 27-FEB-2002 (first entry)
 DT

DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #8122.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 21-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX PI WPI; 2001-639362/73.
 XX DR N-PSDB; AAS72318.
 XX PF New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX PS Claim 20; SEQ ID No 38490; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 104 AA;
 Query Match 3.6%; Score 7; DB 22; Length 104;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 QGLVEAA 173
 Db 87 qglveaa 93
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 RESULT 12
 AAU50142
 ID AAU50142 standard; Protein; 109 AA.
 XX AC AAU50142;
 XX DT 13-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #11038.
 XX DE
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX OS Propionibacterium acnes.
 XX PN WO200181581-A2.
 XX PD 01-NOV-2001.
 XX PF 20-APR-2001; 2001WO-US12865.
 XX PR 21-APR-2000; 2000US-199047P.
 XX PR 02-JUN-2000; 2000US-208841P.
 XX PR 07-JUL-2000; 2000US-216747P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L.maisonneuve J, Zhang Y, Jen S, Carter D;
 XX WPI; 2001-616774/71.
 XX DR N-PSDB; AAS59546.
 XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX PS Example 1; SEQ ID No 11337; 1069pp; English.
 CC Sequences AAU39105-AAU68017 represent propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 109 AA;
 Query Match 3.6%; Score 7; DB 22; Length 109;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 151 TSSPSAR 157
 Db 75 tsspsar 81
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 RESULT 13
 ABG01762
 ID ABG01762 standard; Protein; 129 AA.
 XX AC ABG01762;
 XX DT

DT 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #1753.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR
 PR 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Ermanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS65949.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PT
 XX Claim 20; SEQ ID NO 32121; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 129 AA;
 Query Match 3.6%; Score 7; DB 22; Length 129;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 148 FONTSSP 154
 DB 76 fontssp 82
 RESULT 14
 ABG05157
 ID ABG05157 standard; Protein; 178 AA.
 XX
 AC ABG05157;
 XX
 DT 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #5148.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR
 PR 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS69344.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PT
 XX Claim 20; SEQ ID NO 35516; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 178 AA;
 Query Match 3.6%; Score 7; DB 22; Length 178;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 32 CSRCPPG 38
 DB 35 csrccpg 41
 RESULT 15
 AAG55558
 ID AAG55558 standard; Protein; 211 AA.
 XX
 AC AAG55558;
 XX
 DT 18-OCT-2000 (first entry)
 XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 71260.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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PR 21-APR-1999; 99US-0130449.
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PR 28-APR-1999; 99US-0131449.
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Query Match 3.6%; Score 7; DB 21; Length 211;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TAQSDTT 182
 Db 69 taqsdtt 75

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OM protein - protein search, using sw model

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Title: US-09-299-139A-1
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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	197	100.0	197	2	US-08-505-606-1
2	77	39.1	77	4	US-08-866-545-3
3	10	5.1	415	4	US-09-006-353A-6
4	7	3.6	437	1	US-07-973-324A-6
5	7	3.6	437	1	US-08-343-380-6
6	7	3.6	437	4	US-09-072-435-6
7	7	3.6	437	4	US-09-072-917A-6
8	6	3.0	13	1	US-08-137-016-2
9	6	3.0	14	1	US-08-137-016-3
10	6	3.0	15	1	US-08-137-016-4
11	6	3.0	16	1	US-08-137-016-5
12	6	3.0	17	1	US-08-137-016-6
13	6	3.0	18	1	US-08-137-016-7
14	6	3.0	23	1	US-07-826-928A-11
15	6	3.0	40	1	US-08-129-129-6
16	6	3.0	41	1	US-08-453-924-8
17	6	3.0	44	4	US-09-146-950-8
18	6	3.0	44	4	US-09-146-950-24
19	6	3.0	49	4	US-09-233-506-14
20	6	3.0	114	4	US-09-233-118-1
21	6	3.0	114	4	US-09-233-118-2
22	6	3.0	114	4	US-09-233-118-3
23	6	3.0	137	2	US-08-609-049A-15
24	6	3.0	137	4	US-09-170-996-15
25	6	3.0	147	1	US-08-276-151-4
26	6	3.0	147	1	US-09-527-236A-20
27	6	3.0	155	4	US-09-146-950-4

28	6	3.0	159	4	US-09-146-950-20	Sequence 20, Appl
29	6	3.0	173	4	US-09-133-341-13	Sequence 13, Appl
30	6	3.0	187	2	US-08-713-825-1	Sequence 1, Appl
31	6	3.0	187	3	US-09-199-842-1	Sequence 1, Appl
32	6	3.0	191	3	US-08-906-769-178	Sequence 178, App
33	6	3.0	191	3	US-08-906-616-178	Sequence 178, App
34	6	3.0	191	4	US-08-639-075A-178	Sequence 178, App
35	6	3.0	191	4	US-09-004-731-77	Sequence 77, Appl
36	6	3.0	191	4	US-09-012-431-178	Sequence 178, App
37	6	3.0	191	4	US-08-749-699-77	Sequence 77, Appl
38	6	3.0	191	4	US-09-012-692-178	Sequence 178, App
39	6	3.0	191	4	US-08-906-613-178	Sequence 178, App
40	6	3.0	193	4	US-09-146-950-2	Sequence 2, Appl
41	6	3.0	194	4	US-08-679-493A-215	Sequence 215, App
42	6	3.0	194	4	US-08-679-493A-216	Sequence 216, App
43	6	3.0	197	4	US-09-146-950-18	Sequence 18, Appl
44	6	3.0	217	2	US-08-886-751A-5	Sequence 5, Appl
45	6	3.0	257	1	US-08-077-256-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-505-606-1
; Sequence 1, Application US/08505606
; Patent No. 5925351
; GENERAL INFORMATION:
; APPLICANT: BROWNING, Jeffrey L.
; APPLICANT: BENJAMIN, Christopher D.
; APPLICANT: HOCHMAN, Paula S.
; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
; TITLE OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS
; TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,606
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378,968
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B191
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-505-606-1

Query Match 100.0%; Score 197; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 7.8e-198;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOQAVPPYASNQTCRDEKEYEYEPQHRICCSRCPPGTYVSARKSIRDTVCATCAENS 60
 DB 1 SOQAVPPYASNQTCRDEKEYEYEPQHRICCSRCPPGTYVSARKSIRDTVCATCAENS 60
 QY 61 YNEHWNLYICQLCRPCDPVWGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 DB 61 YNEHWNLYICQLCRPCDPVWGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
 QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAAAGTQSD 180
 DB 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAAAGTQSD 180
 QY 181 TTCKNPLEPLPPMSGT 197
 DB 181 TTCKNPLEPLPPMSGT 197

RESULT 2
 US-08-866-545-3
 ; Sequence 3, Application US/08866545
 ; Patent No. 6265535
 ; GENERAL INFORMATION:
 ; APPLICANT: Greene, Mark I.
 ; APPLICANT: Murali, Ramachandran
 ; APPLICANT: Takasaki, Wataru
 ; TITLE OF INVENTION: PEPTIDES AND PEPTIDE
 ; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
 ; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/866,545
 ; FILING DATE: 30-MAY-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 009113-0004-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 77 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6265535e
 US-08-866-545-3

Query Match 39.1%; Score 77; DB 4; Length 77;
 Best Local Similarity 100.0%; Pred. No. 4.9e-73;

Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHWNLYICQLCRPCDPVWGLEETAPCTSKRKTQCRQCPGMFCAAWALE 111
 DB 1 VCATCAENSYNHWNLYICQLCRPCDPVWGLEETAPCTSKRKTQCRQCPGMFCAAWALE 60
 QY 112 CTHCELLSDCPPGTEAE 128
 DB 61 CTHCELLSDCPPGTEAE 77

RESULT 3
 US-09-006-353A-6
 ; Sequence 6, Application US/09006353A
 ; Patent No. 6261801
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, YING-FEI
 ; APPLICANT: YU, GUO-LIANG
 ; APPLICANT: GENTZ, REINER
 ; APPLICANT: RUBEN, STEVEN
 ; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/006,353A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ANDERS A
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF341
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 415 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-006-353A-6

Query Match 5.1%; Score 10; DB 4; Length 415;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 ARCQPHTRCE 165
 DB 185 ARCQPHTRCE 194

RESULT 4
 US-07-973-324A-6
 ; Sequence 6, Application US/07973324A
 ; Patent No. 5460952
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Su-May
 ; APPLICANT: Liu, Li-Fei
 ; TITLE OF INVENTION: Gene Expression System Comprising the
 ; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,324A
FILING DATE: 04-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-973-324A-6

Query Match 3.6% Score 7; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 GTEAELK 130
|||||
DB 90 GTEAELK 96

RESULT 5
US-08-343-380-6
Sequence 6, Application US/08343380
Patent No. 5712112
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,380
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-380-6

Query Match 3.6% Score 7; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 GTEAELK 130
|||||
DB 90 GTEAELK 96

RESULT 6
US-09-072-435-6
Sequence 6, Application US/09072435
Patent No. 6215051
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-6

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Query Match          3.6%; Score 7; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 GTEAEK 130
DB 90 GTEAEK 96

RESULT 7
US-09-072-917A-6
; Sequence 6, Application US/09072917A
; Patent No. 6288302
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; APPLICANT: Chan, Ming-Tsair
; TITLE OF INVENTION: Application of Alpha-Amylase Gene
; TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
; Patent No. 6288302
; TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
; TITLE OF INVENTION: Plant Seeds
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072.917A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/509,962
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28123/34257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-072-917A-6

Query Match          3.6%; Score 7; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 GTEAEK 130
DB 90 GTEAEK 96

RESULT 8
US-08-137-016-2
; Sequence 2, Application US/08137016
; Patent No. 5494999
; GENERAL INFORMATION:
; APPLICANT: HALE, Geoffrey
; APPLICANT: TONE, Masahide
; APPLICANT: XIA, Meng-Qi
; TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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APPLICANT: HALE, Geoffrey
APPLICANT: TONE, Masahide
APPLICANT: XIA, Meng-Qi
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137.016
FILING DATE: 05-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB 92/00705
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-137-016-2

Query Match          3.0%; Score 6; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 TSSPSA 156
DB 8 TSSPSA 13

RESULT 9
US-08-137-016-3
; Sequence 3, Application US/08137016
; Patent No. 5494999
; GENERAL INFORMATION:
; APPLICANT: HALE, Geoffrey
; APPLICANT: TONE, Masahide
; APPLICANT: XIA, Meng-Qi
; TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: 05-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB 92/00705
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-116
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-137-016-3

Query Match 3.0%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 TSSPSA 156
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Db 8 TSSPSA 13

RESULT 10
US-08-137-016-4
Sequence 4, Application US/08137016
Patent No. 5494999
GENERAL INFORMATION:
APPLICANT: HALE, Geoffrey
APPLICANT: TONE, Masahide
APPLICANT: XIA, Meng-qi
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: 05-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB 92/00705
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.

REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-116
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-137-016-4

Query Match 3.0%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 TSSPSA 156
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Db 8 TSSPSA 13

RESULT 11
US-08-137-016-5
Sequence 5, Application US/08137016
Patent No. 5494999
GENERAL INFORMATION:
APPLICANT: HALE, Geoffrey
APPLICANT: TONE, Masahide
APPLICANT: XIA, Meng-qi
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: 05-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB 92/00705
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-116
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-137-016-5

Query Match 3.0%; Score 6; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 TSSPSA 156
|||||
DB 8 TSSPSA 13

RESULT 12

US-08-137-016-6
; Sequence 6, Application US/08137016
; Patent No. 5494999
; GENERAL INFORMATION:
; APPLICANT: HALE, Geoffrey
; APPLICANT: TONE, Masahide
; APPLICANT: XIA, Meng-Qi
; TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,016
; FILING DATE: 05-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB 92/00705
; FILING DATE: 16-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 91 08056.4
; FILING DATE: 16-APR-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-137-016-6

Query Match 3.0%; Score 6; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 TSSPSA 156
|||||
DB 8 TSSPSA 13

RESULT 13

US-08-137-016-7

; Sequence 7, Application US/08137016
; Patent No. 5494999
; GENERAL INFORMATION:
; APPLICANT: HALE, Geoffrey
; APPLICANT: TONE, Masahide
; APPLICANT: XIA, Meng-Qi
; TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,016
; FILING DATE: 05-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB 92/00705
; FILING DATE: 16-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 91 08056.4
; FILING DATE: 16-APR-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-137-016-7

Query Match 3.0%; Score 6; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 TSSPSA 156
|||||
DB 8 TSSPSA 13

RESULT 14

US-07-826-928A-11
; Sequence 11, Application US/07826928A
; Patent No. 5439829
; GENERAL INFORMATION:
; APPLICANT: Anderson, Leslie D.
; APPLICANT: Cook, James A.
; APPLICANT: David, Gary S.
; APPLICANT: Hochschwender, Susan M.
; APPLICANT: Kashner, Mary S.
; APPLICANT: Smith, Michele C.
; APPLICANT: Stemmer, Willem P.
; TITLE OF INVENTION: METHOD OF IMMOBILIZING AND CROSS LINKING
; PROTEINS AND OTHER MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/826,928A
FILING DATE: 19920124
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Richard B.
REGISTRATION NUMBER: 35,296
REFERENCE/DOCKET NUMBER: X8180A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3589
TELEFAX: 317-276-1294
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-826-928A-11

Query Match 3.0%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 AAGTA 177
|||||
Db 10 AAGTA 15

RESULT 15
US-08-129-129-6
Sequence 6, Application US/08129129
Patent No. 5767363
GENERAL INFORMATION:
APPLICANT: DE SILVA, Jacqueline
APPLICANT: SAFFORD, Richard
APPLICANT: HUGHES, Stephen Glyn
TITLE OF INVENTION: PLANT PROMOTER INVOLVED IN
CONTROLLING LIPID BIOSYNTHESIS IN SEEDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DAREY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,129
FILING DATE: 18-JAN-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91303098.7
FILING DATE: 09-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00627

FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 203424/T7016(C)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-129-129-6

Query Match 3.0%; Score 6; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 80 VMGLEE 85
|||||
Db 4 VMGLEE 9

Search completed: October 4, 2002, 10:16:52
Job time: 220 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2002, 10:15:07 ; Search time 19.61 Seconds
(without alignments)
965.303 Million cell updates/sec

Title: us-09-299-139a-1
Perfect score: 197
Sequence: 1 SQPQAVPPYASENQTCDQEE.....QSDTTCKNPLELPPEMSGT 197

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	197	100.0	435	2	I54182
2	7	3.6	107	2	H97132
3	7	3.6	189	2	C83134
4	7	3.6	265	2	F36914
5	7	3.6	283	2	JC6531
6	7	3.6	283	2	T44579
7	7	3.6	328	2	G86263
8	7	3.6	391	2	T07372
9	7	3.6	437	2	JT0946
10	7	3.6	437	2	JC7138
11	7	3.6	449	2	G82241
12	7	3.6	459	2	G69075
13	7	3.6	474	2	T18904
14	7	3.6	504	2	T35817
15	7	3.6	520	2	A13295
16	7	3.6	580	2	A82447
17	7	3.6	1148	2	S72635
18	7	3.6	1274	2	A89959
19	7	3.6	1753	2	S30855
20	6	3.0	61	2	S18766
21	6	3.0	63	2	D42194
22	6	3.0	63	2	D90762
23	6	3.0	63	2	E85625
24	6	3.0	68	2	T02924
25	6	3.0	75	2	H90913
26	6	3.0	81	2	T09979
27	6	3.0	81	2	E70774
28	6	3.0	87	2	E97642
29	6	3.0	87	2	AG2865

30 acyl carrier prote
31 probable whiB2 pro
32 RNA-binding protei
33 thioredoxin trxA -
34 hypothetical prote
35 thioredoxin - Euba
36 phage-related prot
37 hypothetical prote
38 hypothetical prote
39 hypothetical prote
40 subgroup A Rous sa
41 ribosomal protein
42 ribosomal prote
43 probable membr
44 acyl carrier prote
45 50S ribosomal prot

6 3.0 89 2 C55587
6 3.0 89 2 C70847
6 3.0 93 2 S58674
6 3.0 107 2 S63991
6 3.0 107 2 T49016
6 3.0 110 1 S38989
6 3.0 111 2 C69949
6 3.0 111 2 A85695
6 3.0 112 2 H72682
6 3.0 116 2 G72520
6 3.0 120 2 A48837
6 3.0 124 2 E70148
6 3.0 124 2 G95982
6 3.0 128 2 H97140
6 3.0 129 2 T10175
6 3.0 130 2 AG2468

ALIGNMENTS

RESULT 1

I54182

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000

C:Accession: I54182

R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993

A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq

A:Reference number: I54182; MUID:93252381

A:Accession: I54182

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-435 <RES>

A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762

C:Genetics:

A:Gene: GDB:LTBR

A:Cross-references: GDB:l230195; OMIM:600979

A:Map position: l2p13.3-l2p13.1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 100.0%; Score 197; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.2e-204;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENQTCDQEEYEPQHRICCSRCPPGTYSKCSRIKRDIVCATCAENS 60

Db 28 SQPQAVPPYASENQTCDQEEYEPQHRICCSRCPPGTYSKCSRIKRDIVCATCAENS 87

QY 61 YNEHWNYLTICQLCRPCDPVVMGLEIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 120

Db 88 YNEHWNYLTICQLCRPCDPVVMGLEIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTEAELKDEVGKGNHNCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPTQAQSD 180

Db 148 CPPGTEAELKDEVGKGNHNCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPTQAQSD 207

QY 181 TTCKNPLELPPEMSGT 197

Db 208 TTCKNPLELPPEMSGT 224

RESULT 2

H97132

hypothetical protein CAC1887 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: H97132

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.;

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H97132
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79851.1; PID:g15024867; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1887

Query Match 3.6%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 EXEYEP 26
|||||
Db 83 EXEYEP 89

RESULT 3
C83134
probable pilin PA4086 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83134
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoquchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: C83134
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <STO>
A:Cross-references: GB:AE004825; GB:AE004091; NID:g9950284; PIDN:AAG07473.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4086

Query Match 3.6%; Score 7; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 GLVEAP 174
|||||
Db 142 GLVEAP 148

RESULT 4
F36914
molybdate-binding protein homolog MopA - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C:Accession: F36914
R:Wang, G.; Angermuller, S.; Klipp, W.
J. Bacteriol. 175, 3031-3042, 1993
A:Title: Characterization of Rhodobacter capsulatus genes encoding a molybdenum transpor
A:Reference number: A36914; MUID:93259949
A:Accession: F36914
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <WAN>
A:Note: sequence extracted from NCBI backbone (NCBIN:131915, NCBIP:131921)
C:Superfamily: molybdate-binding protein

Query Match 3.6%; Score 7; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LIVEAPG 175
|||||
Db 66 LIVEAPG 72

RESULT 5
JC6531
avermectin B 5-O-methyltransferase (EC 2.1.1.-) - Streptomyces "avermitilis"
C:Species: Streptomyces "avermitilis"
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
C:Accession: JC6531
R:Ikeda, H.; Wang, L.R.; Ohta, T.; Inokoshi, J.; Omura, S.
Gene 206, 175-180, 1998
A:Title: Cloning of the gene encoding avermectin B 5-O-methyltransferase in avermecti
A:Reference number: JC6531; MUID:98137789
A:Accession: JC6531
A:Molecule type: DNA
A:Residues: 1-283 <IKE>
A:Experimental source: wild type K139
C:Comment: This enzyme catalyzes the methylation of the hydroxyl group at the C5 posi
C:Genetics:
A:Gene: aved
C:Superfamily: bioC homology
C:Keywords: methyltransferase
F:68-172/Domain: bioC homology <BIOC>

Query Match 3.6%; Score 7; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 AAWALEC 112
|||||
Db 138 AAWALEC 144

RESULT 6
T44579
C5-O-methyltransferase [imported] - Streptomyces avermitilis
C:Species: Streptomyces avermitilis
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44579
R:Ikeda, H.; Nonomiya, T.; Usami, M.; Ohta, T.; Omura, S.
Proc. Natl. Acad. Sci. U.S.A. 96, 9509-9514, 1999
A:Title: Organization of the biosynthetic gene cluster for the polyketide anthelminti
A:Reference number: Z22796; MUID:93380548
A:Accession: T44579
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-283 <IKE>
A:Cross-references: EMBL:AB032534; NID:g5921164; PIDN:BAA84602.1; PID:g5921167
C:Genetics:
A:Note: aved

Query Match 3.6%; Score 7; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 AAWALEC 112
|||||
Db 138 AAWALEC 144

RESULT 7
G86263
hypothetical protein F3F19.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: G86263
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719
 A:Accession: G86263
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-328 <STO>
 A:Cross-references: GB:AE005172; NID:94850382; PIDN:AA031052.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 3.6%; Score 7; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 SPSARC 158
 Db 132 SPSARC 138
 |||||

RESULT 8

T07372
 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) E1 alpha chain - potato
 C:Species: Solanum tuberosum (potato)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: T07372
 R:Grof, C.P.; Winning, B.M.; Scaysbrook, T.P.; Hill, S.A.; Leaver, C.J.
 Plant Physiol. 108, 1623-1629, 1995
 A:Title: Mitochondrial pyruvate dehydrogenase. Molecular cloning of the E1 alpha subunit
 A:Reference number: Z15993; MUID:95388769
 A:Accession: T07372
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-391 <GRO>
 A:Cross-references: EMBL:Z26949; NID:9473168; PIDN:CAA81558.1; PID:9473169
 A:Experimental source: cv. Desiree; tissue type leaf
 C:Genetics:
 A:Genome: nuclear
 A:Complex: heterotetramer; two alpha and two beta chains
 C:Function:
 A:Description: catalyzes the initial oxidative decarboxylation of pyruvate and converts
 C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin
 C:Keywords: flavoprotein; heterotetramer; mitochondrion; oxidoreductase; thiamin pyropho
 F:187-236/domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 3.6%; Score 7; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 TEALKD 131
 Db 332 TEALKD 338
 |||||

RESULT 9

JT0946
 alpha-amylase 3E - rice
 C:Species: Oryza sativa (rice)
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000
 C:Accession: JT0946
 R:Huang, N.; Koizumi, N.; Reinl, S.; Rodriguez, R.L.
 Nucleic Acids Res. 18, 7007-7014, 1990
 A:Title: Structural organization and differential expression of rice alpha-amylase genes
 A:Reference number: JT0945; MUID:9108278
 A:Accession: JT0946

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-437 <HUA>
 A:Cross-references: GB:M59352; GB:M36985; NID:g169772; PIDN:AAA33896.1; PID:g169773
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 F:171-315/domain: alpha-amylase core homology <AMY>

Query Match 3.6%; Score 7; DB 2; Length 437;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 GTEALK 130
 Db 90 GTEALK 96
 |||||

RESULT 10

JC7138
 alpha-amylase (EC 3.2.1.1) isozyme III - rice
 N:Alternate names: 1,4-gulcan glucanohydrolase III
 C:Species: Oryza sativa (rice)
 C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
 C:Accession: JC7138; PC7040
 R:Abe, R.; Yoshida, K.; Aoyagi, M.; Kasahara, S.; Ichishima, E.; Nakajima, T.
 Biosci. Biotechnol. Biochem. 63, 1329-1335, 1999
 A:Title: Characterization of chimeric enzymes constructed between two distinct alpha-
 A:Reference number: JC7137; MUID:99430781
 A:Accession: JC7138
 A:Molecule type: mRNA
 A:Residues: 1-437 <ABE>
 A:Accession: PC7040
 A:Molecule type: protein
 A:Residues: 246-253 <AB2>
 C:Comment: This enzyme catalyzes the hydrolysis of internal alpha-glucosidic linkages
 is important in germinating seeds and presenting as multiple isoforms.
 C:Genetics:
 A:Gene: amy-III
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: calcium binding; germination; glycosidase; hydrolase; seed

Query Match 3.6%; Score 7; DB 2; Length 437;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 GTEALK 130
 Db 90 GTEALK 96
 |||||

RESULT 11

G82241
 conserved hypothetical protein VC1108 [imported] - Vibrio cholerae (strain N16961 ser
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: G82241
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
 I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833
 A:Accession: G82241
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-449 <H1>
 A:Cross-references: GB:AE004191; GB:AE003852; NID:g9655568; PIDN:AAF94267.1; GSPDB:GN

A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC1108
 A:Map position: 1
 C:Superfamily: Haemophilus influenzae conserved hypothetical protein HI1590

Query Match 3.6%; Score 7; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 PPEMSGT 197
|||||||
DB 408 PPEMSGT 414

RESULT 12

G69075
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Jun-1999
C:Accession: G69075
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: AG9000; MUID:98037514
A:Accession: G69075
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-459 <MTH>
A:Cross-references: GB:AE000916; GB:AE000666; NID:G2622674; PIDN:AAB86038.1; PID:G262268
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1564
C:Superfamily: dinitrogenase beta chain

Query Match 3.6%; Score 7; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EYEPQH 28
|||||||
DB 448 EYEPQH 454

RESULT 13

T18904
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18904
R:Lloyd, C.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z19042
A:Accession: T18904
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-474 <WIL>
A:Cross-references: EMBL:Z69716; PIDN:CAA93527.1; GSPDB:GN00028; CESP:C04B4.2
C:Genetics:
A:Gene: CFSP:C04B4.2
A:Map position: X
A:Introns: 67/3; 161/2; 207/3; 435/1

Query Match 3.6%; Score 7; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GTYVSAK 44
|||||||
DB 275 GTYVSAK 281

RESULT 14

T35817
probable Glu-tRNA(Gln) amidotransferase chain B - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C:Accession: T35817
R:Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, February 1999
A:Reference number: Z21589
A:Accession: T35817
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-504 <MOR>
A:Cross-references: EMBL:AL035569; PIDN:CAB37577.1; GSPDB:GN00070; SCODEB:SC8D9.13
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: gatB; SCODEB:SC8D9.13
C:Superfamily: PET112 protein

Query Match 3.6%; Score 7; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 DPVMGLE 84
|||||||
DB 18 DPVMGLE 24

RESULT 15

AI3295
adenylosuccinate synthetase (EC 6.3.4.4) [imported] - Brucella melitensis (strain 16M
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AI3295
R:DeIvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AI3295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL51532.1; PID:G17982249; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0351
A:Map position: I
C:Keywords: ligase

Query Match 3.6%; Score 7; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 MGLEIEIA 87
|||||||
DB 266 MGLEIEIA 272

Search completed: October 4, 2002, 10:17:19
Job time: 132 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2002, 10:16:57 ; Search time 11.95 Seconds
(without alignments)
638.306 Million cell updates/sec

Title: US-09-299-139A-1
Perfect score: 197
Sequence: 1 SQQAVPPASENQTCDQEE.....QSDTTCKNPLELPPEMSGT 197

Scoring table:
OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	197	100.0	435	1	TNR3_HUMAN
2	10	5.1	415	1	TNR3_MOUSE
3	7	3.6	176	1	IF3_STRPY
4	7	3.6	265	1	MOPA_RHOCA
5	7	3.6	391	1	ODPA_SOLTU
6	7	3.6	402	1	PURA_BRUAB
7	7	3.6	437	1	AM3E_ORYSA
8	7	3.6	459	1	NIFK_METH
9	7	3.6	459	1	NIFK_METH
10	7	3.6	504	1	GATB_STRCO
11	7	3.6	646	1	WEEL_RAT
12	7	3.6	1753	1	YEW2_YEAST
13	6	3.0	61	1	CD52_HUMAN
14	6	3.0	63	1	YPH2_SYNP2
15	6	3.0	81	1	ATPL_MYCLE
16	6	3.0	81	1	ATPL_MYCTU
17	6	3.0	81	1	VMD2_MOUSE
18	6	3.0	107	1	THIO_CLOLI
19	6	3.0	110	1	THIO_EUBAC
20	6	3.0	111	1	YQCD_BACSU
21	6	3.0	124	1	RL7_BORBU
22	6	3.0	129	1	ACP2_HORVU
23	6	3.0	129	1	RR12_GUITH
24	6	3.0	132	1	ACP3_HORVU
25	6	3.0	134	1	ACP1_BRANA
26	6	3.0	134	1	ACP2_BRANA
27	6	3.0	134	1	ACP3_BRANA
28	6	3.0	134	1	ACP5_BRANA
29	6	3.0	134	1	ACP_BRACM
30	6	3.0	134	1	YHCB_HAEIN
31	6	3.0	135	1	ACP1_CASGL
32	6	3.0	137	1	ACP1_ARATH
33	6	3.0	137	1	ACP2_CUPLA

RESULT 1

ID	TNR3_HUMAN	STANDARD;	PRT;	435 AA.
AC	P36941;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Lymphotoxin-beta receptor precursor (Tumor necrosis factor receptor)			
DE	2 related protein) (Tumor necrosis factor C receptor).			
GN	LTBR OR TNFR OR TNFRSF3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver.			
EX	MEDLINE=93252381; PubMed=8486360;			
RA	Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;			
RT	"Construction and evaluation of a hncDNA library of human l2p			
RT	transcribed sequences derived from a somatic cell hybrid.";			
RL	Genomics 16:214-218(1993).			
RN	[2]			
RP	FUNCTION.			
RA	MEDLINE=94225209; PubMed=8171323;			
RA	Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,			
RA	Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;			
RT	"A lymphotoxin-beta-specific receptor.";			
RL	Science 264:707-710(1994).			
CC	-1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN			
CC	IMMUNE DEVELOPMENT.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
CC	-----			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; L04270; AAA36757.1; -			
DR	HSSP; P25942; 1CDF.			
DR	MIN; 600979; -			
DR	InterPro; IPR001368; TNFR_c6; 4.			
DR	Pfam; PF00020; TNFR_c6; 4.			
DR	ProDom; PD000771; TNFR_c6; 1.			
DR	SMART; SM00208; TNFR; 4.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 3.			
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal.			
FT	SIGNAL 1 30 POTENTIAL.			
FT	CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.			
FT	DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 228 248 POTENTIAL.			

34	6	3.0	139	1	ACP4_CUPLA	P52414	cuphea lanc
35	6	3.0	140	1	ACP1_CUPLA	P52411	cuphea lanc
36	6	3.0	142	1	NIU2_RHOCA	Q10373	rhodobacter
37	6	3.0	143	1	ACP3_CUPLA	P52413	cuphea lanc
38	6	3.0	143	1	PP1B_BACSU	P35137	bacillus su
39	6	3.0	149	1	ACP1_HORVU	P02902	hordeum vul
40	6	3.0	149	1	NDK1_ORYSA	Q07661	oryza sativ
41	6	3.0	151	1	NDK_ARCFU	O29491	archaeoglob
42	6	3.0	151	1	ACP2_ARATH	P25701	arabidopsis
43	6	3.0	157	1	RA05_ORYSA	Q01881	oryza sativ
44	6	3.0	157	1	RSVR_COTJA	P98162	coturnix co
45	6	3.0	158	1	ACP3_ARATH	P25702	arabidopsis

ALIGNMENTS

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FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 62462656022F656F CRC64;

Query Match 100.0%; Score 197; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 8.3e-202; Indels 0; Gaps 0;
Matches 197; Conservative 0; Mismatches 0;

QY 1 SQQAVPPYASNTCRDQKEYEPQHRICCSRCPPGYVSAAKSRIRDTVCATCAENS 60
DB 28 SQQAVPPYASNTCRDQKEYEPQHRICCSRCPPGYVSAAKSRIRDTVCATCAENS 87
QY 61 YNEHNYLTICQLRCPDVPVGLIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHNYLTICQLRCPDVPVGLIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPTGEAEKLDVGGNNHCVCCKAGHFONTSSPSARCOPHTRCENOGVLEAAPTGAQSD 180
DB 148 CPPTGEAEKLDVGGNNHCVCCKAGHFONTSSPSARCOPHTRCENOGVLEAAPTGAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 2
ID TNR3_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Lymphotoxin-beta receptor precursor.
GN LTBR OR TNFR OR TNFRSF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping."
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
```

```

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL; U29173; AAA68964.1; -
DR EMBL; L38423; AAB00846.1; -
DR EMBL; U30798; AAA81334.1; -
DR HSSP; P25942; 1CDF.
DR MGD; MGI:104875; Ltbr.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 170 TNFR-CYS 3.
FT REPEAT 171 213 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 5.1%; Score 10; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 ARCQPHTRCE 165
DB 185 ARCQPHTRCE 194

RESULT 3
ID IF3_STRPY STANDARD; PRT; 176 AA.
AC P58081;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Translation initiation factor IF-3.
GN INFC OR SPY0804.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
```

RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
RT "Complete genome sequence of an M1 strain of Streptococcus
RT pyogenes";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE
CC EQUILIBRIUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN
CC FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S
CC SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
CC -----
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CC -----
DR EMBL; AE006531; AAK33741.1; -
DR InterPro; IPR001288; IF3.
DR Pfam; PF00707; IF3; 1.
DR ProDom; PD002880; IF3; 1.
DR PROSITE; PS00938; IF3; 1.
KW Initiation factor; Protein biosynthesis; Complete proteome.
SQ SEQUENCE 176 AA; 20053 MW; FD3247FB6C9D5919 CRC64;

Query Match 3.6%; Score 7; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPQAVPP 8
Db 53 QPQAVPP 59
|||||||

RESULT 4
MOPA_RHOCA STANDARD; PRT; 265 AA.
AC Q08385;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Molybdenum-pterin binding protein mopa.
GN MOPA.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33303 / B10;
RX MEDLINE=93259949; PubMed=8491722;
RA Wang G., Angermueller S., Klipp W.,
RT "Characterization of Rhodobacter capsulatus genes encoding a
RT molybdenum transport system and putative molybdenum-pterin-binding
RT proteins";
RL J. Bacteriol. 175:3031-3042(1993).
CC -!- SIMILARITY: BELONGS TO THE MOPA FAMILY.
CC -----
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DR

DR EMBL; L06254; AAA71912.1; -
DR InterPro; IPR003725; Mode.
DR Pfam; PF02573; Mode; 1.
KW Transport; Molybdenum; Repeat.
FT REPEAT 125 192 MOP-LIKE.
FT REPEAT 193 265 MOP-LIKE.
SQ SEQUENCE 265 AA; 27119 MW; 7EB89FC938CAF326 CRC64;

Query Match 3.6%; Score 7; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 LVEAAPG 175
Db 66 LVEAAPG 72
|||||||

RESULT 5
ODPA_SOLITU STANDARD; PRT; 391 AA.
AC P52903;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial
DE precursor (EC 1.2.4.1) (PDHE1-A).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DESIREE; TISSUE=Leaf;
RX MEDLINE=95386769; PubMed=7659754;
RA Grof C.P., Wanning B.M., Scaysbrook T.P., Hill S.A., Leaver C.J.;
RT "Mitochondrial pyruvate dehydrogenase. Molecular cloning of the E1
RT alpha subunit and expression analysis";
RL Plant Physiol. 108:1623-1629(1995).
RN [2]
RP SEQUENCE OF 27-42.
RC STRAIN=CV. ROMANO; TISSUE=Tuber;
RX MEDLINE=98399821; PubMed=9729464;
RA Millar A.H., Knorr C., Leaver C.J., Hill S.A.;
RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and
RT identification of catalytic components in potato";
RL Biochem. J. 334:571-576(1998).
CC -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
CC CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
CC COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
CC DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
CC (E3).
CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
CC acetyldihydrolipoamide + CO(2).
CC -!- COFACTOR: THIAMINE PYROPHOSPHATE.
CC -!- ENZYME REGULATION: E1 ACTIVITY IS REGULATED BY PHOSPHORYLATION
CC (INACTIVATION) AND DEPHOSPHORYLATION (ACTIVATION) OF THE ALPHA
CC SUBUNIT (BY SIMILARITY).
CC -!- SUBUNIT: Tetramer of two alpha and two beta subunits (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z26949; CAA81558.1; -
DR InterPro; IPR001017; E1_dh.

DR Pfam; PF00676; EL_dehydrog; 1.
KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
FT Phosphorylation; Mitochondrion; Transit peptide.
FT TRANSIT 1 26 MITOCHONDRION
FT CHAIN 27 391 PYRUVATE DEHYDROGENASE E1 COMPONENT
FT ALPHA SUBUNIT.
SQ SEQUENCE 391 AA; 43228 MW; F9110B374B022F0D CRC64;

Query Match 3.6%; Score 7; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 125 TEALKLD 131
DB 332 TEALKLD 338
|||||||

RESULT 6
PURA_BRUAB STANDARD; PRT; 402 AA.
AC P52004;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
DE (ADSS) (AMPSase) (Fragment).
GN PURA.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2308;
RA Tatum F.M., Steckelberg M.A.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
[2]
RP IDENTIFICATION OF A PROBABLE C-TERMINAL FRAMESHIFT.
RA Michoud K.;
RL Unpublished observations (NOV-1999).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE DE NOVO PATHWAY OF PURINE
NUCLEOTIDE BIOSYNTHESIS.
CC -!- CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP + phosphate +
adenylosuccinate.
CC -!- PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
CC -!- SIMILARITY: BELONGS TO THE ADENYLOSUCCINATE SYNTHETASE FAMILY.

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DR EMBL; L43054; AAA75455.1; -
DR HSPR; P12283; 1ADE.
DR InterPro; IPR001114; Adenylsucc_synth.
DR Pfam; PF00709; Adenylsucc_synth; 1.
DR ProDom; PD001188; Adenylsucc_synth; 1.
DR PROSITE; PS00513; ADENYLOSUCCIN_SVN_2; 1.
DR PROSITE; PS01266; ADENYLOSUCCIN_SVN_1; 1.
KW Purine biosynthesis; Ligase; GTP-binding.
FT NP_BIND 12 18
FT ACT_SITE 140 140 BY SIMILARITY.
FT ACT_SITE 147 147 BY SIMILARITY.
FT CONFLICT 393 402 XKYVRHIEEL -> SNMSAISK (IN REF. 1).
FT NON_TER 402 402
SQ SEQUENCE 402 AA; 43919 MW; F443CFAE8D10EE75 CRC64;

Query Match 3.6%; Score 7; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 MGLEEIA 87
DB 175 MGLEEIA 181
|||||||

RESULT 7
AM3E_ORYSA STANDARD; PRT; 437 AA.
ID AM3E_ORYSA
AC P27934;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Alpha-amylase isozyme 3E precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
DE GN AMY1.4 OR AMY3E.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. JAPONICA M202; TISSUE=Etiolated leaf;
RX MEDLINE=91088278; PubMed=2263460;
RA Huang N., Koizumi N., Reini S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
amylase genes.";
RL Nucleic Acids Res. 18:7007-7014(1990).
CC -!- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
GERMINATION.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -!- SUBUNIT: MONOMER.
CC -!- TISSUE SPECIFICITY: MORE ABUNDANT IN GERMINATING SEEDS THAN IN
YOUNG ROOTS, YOUNG LEAVES AND CALLUS.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.

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DR EMBL; M59352; AAA33896.1; -
DR PIR; JT0946; JT0946.
DR HSPR; P04063; 1AVA.
DR Mendel; 9691; Orysa; Amy1.4.
DR InterPro; IPR000461; Alpha_amylase.
DR Pfam; PF0128; alpha-amylase; 1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 437 ALPHA-AMYLASE ISOZYME 3E.
FT ACT_SITE 204 204 BY SIMILARITY.
FT ACT_SITE 312 312 BY SIMILARITY.
FT CA_BIND 116 116 BY SIMILARITY.
FT CA_BIND 175 175 BY SIMILARITY.
SQ SEQUENCE 437 AA; 48707 MW; C0E8276CCEA16602 CRC64;

Query Match 3.6%; Score 7; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 124 GTEAEK 130
Db 90 GTEAEK 96

RESULT 8
NIFK_METTH
ID NIFK_METTH STANDARD; PRT; 459 AA.
AC O27606;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nitrogenase molybdenum-iron protein beta chain (EC 1.18.6.1)
DE (Nitrogenase component I) (Dinitrogenase).
GN NIFK OR MTH1564.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Saffer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- FUNCTION: THE KEY ENZYMIC REACTIONS IN NITROGEN FIXATION ARE
CC CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
CC IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
CC -1- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP
CC = 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.
CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
CC 30-32 FE, 2 MO, AND INORGANIC SULFUR.
CC -1- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
CC -----
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CC -----
DR EMBL; X87971; CAA61220.1;
DR HSSP; P11347; IMIO.
DR InterPro; IPR000318; Nitrogense_compl.
DR InterPro; IPR000510; Oxidored_nitrogense_1.
DR Pfam; PF00148; oxidored_nitro; 1.
DR PROSITE; PS00090; NITROGENASE_1.2; 1.
DR PROSITE; PS00699; NITROGENASE_1.1; 1.
DR Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
KW Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
SQ SEQUENCE 459 AA; 51158 MW; 04FC3EA9CE3E9E37 CRC64;

Query Match 3.6%; Score 7; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EYEPQH 28
Db 448 EYEPQH 454

RESULT 10
GATB_STRCO
ID GATB_STRCO STANDARD; PRT; 504 AA.
AC O92578;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-) (Glu-ADT
DE subunit B).
GN GATB OR SC8D9.13.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Murphy L., Harris D., Bentley S.D., Parkhill J., Barrell B.G.,
RA Rajandream M.A.;

Query Match 3.6%; Score 7; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EYEPQH 28
Db 448 EYEPQH 454

RESULT 9

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Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 -!- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED GLN-TRNA(GLN) THROUGH THE TRANSAMINATION OF MISACYLATED GLU-TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
 -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE = ADP + PHOSPHATE + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMATE.
 -!- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
 -!- SIMILARITY: BELONGS TO THE GATB FAMILY.

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 DR EMBL; AL035569; CAB37577.1; -
 DR InterPro; IPR003789; DUF186.
 DR InterPro; IPR001773; Gln_amidotransf_B.
 DR Pfam; PF02637; DUF186; 1.
 DR Pfam; PF01162; GatB; 1.
 DR Pfam; PF02934; GatB_N; 1.
 DR PROSITE; PS01234; GATB; 1.
 KW Protein biosynthesis; Ligase.
 SQ SEQUENCE 504 AA; 54495 MW; 7B05B23268146CDA CRC64;

Query Match 3.6%; Score 7; DB 1; Length 504;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 DPVVGLE 84
 |||||
 DB 18 DPVVGLE 24

RESULT 11
 WEEL_RAT
 ID WEEL_RAT STANDARD; PRT; 646 AA.
 AC Q63802;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Weel-like protein kinase (EC 2.7.1.112).
 GN WEEL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Furunobu A.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY ACT AS A NEGATIVE REGULATOR OF ENTRY INTO MITOSIS (G2 TO M TRANSITION) BY PROTECTING THE NUCLEUS FROM CYTOPLASMICALLY ACTIVATED CYCLIN B1-COMPLEXED CDC2 BEFORE THE ONSET OF MITOSIS. ITS ACTIVITY INCREASES DURING S AND G2 PHASES AND DECREASES AT M PHASE WHEN IT IS HYPERPHOSPHORYLATED. A CORRELATED DECREASE IN PROTEIN LEVEL OCCURS AT M/G1 PHASE, PROBABLY DUE TO ITS DEGRADATION. SPECIFICALLY PHOSPHORYLATED AND INACTIVATES CYCLIN B1-COMPLEXED CDC2 REACHING A MAXIMUM DURING G2 PHASE AND A MINIMUM AS CELLS ENTER M PHASE. PHOSPHORYLATION OF CYCLIN B1-CDC2 OCCURS EXCLUSIVELY ON TYR-15 AND PHOSPHORYLATION OF MONOMERIC CDC2 DOES NOT OCCUR (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -!- ENZYME REGULATION: SYNTHESIS IS INCREASED DURING S AND G2 PHASES, PRESUMABLY BY AN INCREASE IN TRANSCRIPTION; ACTIVITY IS DECREASED BY PHOSPHORYLATION DURING M PHASE. PROTEIN LEVELS FALL IN M PHASE AS A RESULT OF DECREASED SYNTHESIS COMBINED WITH DEGRADATION.

ACTIVITY SEEMS TO BE NEGATIVELY REGULATED BY PHOSPHORYLATION UPON ENTRY INTO MITOSIS, ALTHOUGH N-TERMINAL PHOSPHORYLATION MIGHT ALSO REGULATE THE PROTEIN STABILITY VIA PROTECTION FROM PROTEOLYSIS OR MIGHT REGULATE THE SUBCELLULAR LOCATION (BY SIMILARITY).
 -!- SUBUNIT: BINDS TO 14-3-3 PROTEIN ZETA.
 -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 -!- PTM: PHOSPHORYLATED DURING M AND G1 PHASES. ALSO AUTOPHOSPHORYLATED (By similarity).
 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. WEEL SUBFAMILY.

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 DR EMBL; D31838; BAA06624.1; -
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Mitosis; Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Nuclear protein.
 KW DOMAIN 34 42 POLY-GLU.
 FT DOMAIN 74 77 POLY-ARG.
 FT DOMAIN 97 101 POLY-GLY.
 FT DOMAIN 298 568 PROTEIN KINASE.
 -FT NP_BIND 304 312 ATP (BY SIMILARITY).
 FT BINDING 327 327 ATP (BY SIMILARITY).
 FT ACT_SITE 425 425 BY SIMILARITY.
 FT MOD_RES 123 123 PHOSPHORYLATION (BY CDC2) (POTENTIAL).
 FT MOD_RES 139 139 PHOSPHORYLATION (BY CDC2) (POTENTIAL).
 SQ SEQUENCE 646 AA; 71496 MW; 740120F51C811DAF CRC64;

Query Match 3.6%; Score 7; DB 1; Length 646;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TEAEKLD 131
 |||||
 DB 398 TEAEKLD 404

RESULT 12
 YEW2_YEAST
 ID YEW2_YEAST STANDARD; PRT; 1753 AA.
 AC P32634;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Hypothetical 195.4 kDa protein in RPS26B-GLC7 intergenic region.
 GN YER132C OR SVGP-ORF50.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C., Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,

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RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.,
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO S.POMBE RAL2.
CC -1- SIMILARITY: TO YEAST MDS3.
CC
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CC -----
CC DR EMBL; U18916; AAC03230.1; -.
CC DR PIR; S30855; S30855.
CC DR SGD; S0000934; PMD1.
CC DR InterPro; IPR001798; Kelch.
CC DR Pfam; PF01344; Kelch; 2.
CC DR Hypothetical protein.
CC SQ SEQUENCE 1753 AA; 195382 MW; E4252998C6C2508B CRC64;
CC
CC Query Match 3.68; Score 7; DB 1; Length 1753;
CC Best Local Similarity 100.0%; Pred. No. 42;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 186 PLEPLPP 192
CC |||||
CC DB 938 PLEPLPP 944
CC
CC RESULT 13
CC CD52_HUMAN
CC ID CD52_HUMAN STANDARD; PRT; 61 AA.
CC AC P31358;
CC DT 01-JUL-1993 (Rel. 26, Created)
CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE CAMPATH-1 antigen precursor (CD52 antigen) (CDW52) (Cambridge
CC DE pathology 1 antigen) (Epididymal secretory protein E5).
CC GN CD52 OR HE5.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-35.
CC RC TISSUE=Splice;
CC RX MEDLINE=91285018; PubMed=1711975;
CC RA Xia M.-Q., Tone M., Packman L., Hale G., Waldmann H.;
CC RT "Characterization of the CAMPATH-1 (CDw52) antigen: biochemical
CC RT analysis and cDNA cloning reveal an unusually small peptide
CC RT backbone.;"
CC RL Eur. J. Immunol. 21:1677-1684(1991).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RP TISSUE=Epididymis;
CC RX MEDLINE=93119668; PubMed=8418821;
CC RA Kirchhoff C., Krull N., Pera I., Ivell R.;
CC RT "A major mRNA of the human epididymal principal cells, HE5, encodes
CC RT the leucocyte differentiation CDw52 antigen peptide backbone.;"
CC RL Mol. Reprod. Dev. 34:8-15(1993).
CC -1- FUNCTION: MAY PLAY A ROLE IN CARRYING AND ORIENTING CARBOHYDRATE,
CC AS WELL AS HAVING A MORE SPECIFIC ROLE.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD52 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd52.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; X62466; CAA44323.1; -.
CC DR EMBL; X67699; CAA47929.1; -.
CC DR EMBL; A23013; CAA01644.1; -.
CC DR PIR; S18766; S18766.
CC DR MIM; 114280; -.
CC KW Antigen; Signal; Glycoprotein; GPI-anchor; Membrane; Polymorphism.
CC FT SIGNAL 1 24
CC FT CHAIN 25 36
CC FT PROPEP 37 61
CC FT LIPID 36 36
CC FT CARBOHYD 27 27
CC FT CARBOHYD 40 40
CC FT VARIANT 40 41
CC FT NI-> SM.
CC FT SEQUENCE 61 AA; 6614 MW; 4AE2A056682BEEA6 CRC64;
CC /FTID=VAR_005130.
CC
CC Query Match 3.08; Score 6; DB 1; Length 61;
CC Best Local Similarity 100.0%; Pred. No. 25;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 151 TSSPSA 156
CC |||||
CC DB 32 TSSPSA 37
CC
CC RESULT 14
CC YPH2_SYNP2
CC ID YPH2_SYNP2 STANDARD; PRT; 63 AA.
CC AC P32040;
CC DT 01-JUL-1993 (Rel. 26, Created)
CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
CC DT 01-MAR-2002 (Rel. 41, Last annotation update)
CC DE Hypothetical protein in petH 3' region (Fragment).
CC OS Synecococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
CC OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
CC OX NCBI_TaxID=32049;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=92207922; PubMed=1554697;
CC RA Schluchter W.M., Bryant D.A.;
CC RT "Molecular characterization of ferredoxin-NADP+ oxidoreductase in
CC RT cyanobacteria: cloning and sequence of the petH gene of Synecococcus
CC RT sp. PCC 7002 and studies on the gene product.;"
CC RL Biochemistry 31:3092-3102(1992).
CC CC -1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
CC
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CC -----
CC DR EMBL; M86234; AAA27325.1; -.
CC DR PIR; D42194; D42194.
CC DR InterPro; IPR001789; Response_reg.
CC DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
CC KW Hypothetical protein; Sensory transduction.
CC FT DOMAIN 20 >63 RESPONSE REGULATORY.
CC FT NON_TER 63 63
CC SQ SEQUENCE 63 AA; 7142 MW; A9F58D9E01180896 CRC64;
CC
CC Query Match 3.08; Score 6; DB 1; Length 63;
CC Best Local Similarity 100.0%; Pred. No. 26;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Length 81;
QY 80 VMGLEE 85 ||||| Best Local Similarity 3.0%; Score 6; DB 1; DB 1;
Db 35 VMGLEE 40 ||||| Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

ATPL_MYCLE

ID ATPL_MYCLE STANDARD; PRT; 81 AA.

AC P45828;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE ATP synthase C chain (EC 3.6.3.14) (Lipid-binding protein)

DE (Dicyclohexylcarbodiimide-binding protein).

GN ATPE OR ML1140.

OS Mycobacterium leprae.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1769;

RN [1]

RP SEQUENCE FROM N.A.

RA Smith D.R., Robison K.;

RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-TN;

RX MEDLINE=21128732; PubMed=11234002;

RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,

RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RA Barrell B.G.;

RT "Massive gene decay in the leprosy bacillus.";

RL Nature 409:1007-1011(2001).

CC -!- FUNCTION: THIS IS ONE OF THE THREE CHAINS OF THE NONENZYMATIC

CC -!- COMPONENT (CF(0) SUBUNIT) OF THE ATPASE COMPLEX.

CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC

CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE

CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)

CC HAS THREE MAIN SUBUNITS: A, B AND C.

CC -!- MISCELLANEOUS: DICYCLOHEXYLCARBODIIMIDE (DCDD) INHIBITS ATPASE.

CC -!- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.

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CC -----

DR EMBL; U15186; AA63107.1; -

DR EMBL; AL583920; CAC31521.1; -

DR HSP; P00844; I491.

DR Leproma; ML1140; -

DR InterPro; IPR002379; ATPase_C.

DR InterPro; IPR000454; ATPase_C_eub.

DR Pfam; PF00137; ATP-synt_C; 1

DR PROSITE; PS00605; ATPASE_C; 1.

KW Hydrogen ion transport; CF(0); Transmembrane; Lipid-binding;

KW Complete proteome.

FT TRANSMEM 5 25 POTENTIAL.

FT TRANSMEM 57 77 POTENTIAL.

FT BINDING 61 61 DICYCLOHEXYLCARBODIIMIDE (BY SIMILARITY).

SQ SEQUENCE 81 AA; 8205 MW; E5456207EE9E0C13 CRC64;

Search completed: October 4, 2002, 10:20:49

Job time: 232 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2002, 10:16:37 ; Search time 26.57 Seconds
(without alignments)
1282.650 Million cell updates/sec

Title: US-09-299-139A-1
Perfect score: 197

Sequence: 1 SQQAVPPYASENQTCDQE.....QSDTTCKNPLEPLPMSGT 197

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL19.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	7	3.6	107	16 Q97HW9	Q97hw9 clostridium
2	7	3.6	150	17 Q96YM2	Q96ym2 sulfolobus
3	7	3.6	189	16 Q9HWU2	Q9hwu2 pseudomonas
4	7	3.6	204	2 Q93J78	Q93j78 streptomyce
5	7	3.6	266	4 Q9H611	Q9h611 homo sapien
6	7	3.6	283	2 Q9S0N6	Q9s0n6 streptomyce
7	7	3.6	302	13 Q9PU50	Q9pus0 salvelinus
8	7	3.6	327	5 Q9GPD4	Q9gpd4 trypanosoma
9	7	3.6	328	10 Q9SAD4	Q9sad4 arabidopsis
10	7	3.6	370	4 Q12953	Q12953 homo sapien
11	7	3.6	371	12 Q9DJR1	Q9djr1 citrus tris
12	7	3.6	391	10 Q9FR11	Q9fr11 lycopersico
13	7	3.6	392	2 Q52181	Q52181 synecocyst
14	7	3.6	412	16 Q92RW6	Q92rw6 rhizobium m
15	7	3.6	432	17 Q97CE9	Q97ce9 thermoplasm
16	7	3.6	449	16 Q9KSZ8	Q9ksz8 vibrio chol

17	7	3.6	474	5 Q17G20	Q17g20 caenorhabdi
18	7	3.6	485	2 Q9L2L1	Q9l2l1 streptomyce
19	7	3.6	500	2 Q9RXK6	Q9rxk6 streptomyce
20	7	3.6	555	10 Q94LS5	Q94ls5 oryza sativ
21	7	3.6	580	16 Q9KM44	Q9km44 vibrio chol
22	7	3.6	619	4 Q9H5G7	Q9h5g7 homo sapien
23	7	3.6	629	4 Q9UI92	Q9ui92 homo sapien
24	7	3.6	647	4 Q96031	Q96031 homo sapien
25	7	3.6	668	4 Q9H5C7	Q9h5c7 homo sapien
26	7	3.6	751	11 Q924I0	Q924i0 mus musculu
27	7	3.6	751	11 Q921D6	Q921d6 mus musculu
28	7	3.6	760	5 Q9VTA3	Q9vta3 drosophila
29	7	3.6	840	11 Q9DC40	Q9dvc40 mus musculu
30	7	3.6	840	11 Q91VQ3	Q91vg3 mus musculu
31	7	3.6	1148	2 Q60045	Q60045 thermoanaer
32	7	3.6	1274	16 Q99TC3	Q99tc3 staphylococ
33	7	3.6	1307	4 Q9C093	Q9c093 homo sapien
34	7	3.6	1365	4 Q96028	Q96028 homo sapien
35	7	3.6	1744	11 Q9R095	Q9r095 rattus norv
36	7	3.6	1886	5 Q9NRU5	Q9nku5 leishmania
37	7	3.6	2000	12 Q9Q8G7	Q9q8g7 myxococcus
38	7	3.6	2393	2 Q925F4	Q925f4 myxococcus
39	7	3.6	2554	5 Q9NKT1	Q9nkt1 leishmania
40	7	3.6	2654	13 Q9DE14	Q9del4 xenopus lae
41	7	3.6	3939	2 Q93HJ3	Q93hj3 streptomyce
42	7	3.6	4360	3 Q9UVN5	Q9uvn5 alternaria
43	6	3.0	22	4 Q9UCH8	Q9uch8 homo sapien
44	6	3.0	50	2 Q9F0N6	Q9f0n6 bacillus am
45	6	3.0	61	4 Q9BW46	Q9bw46 homo sapien

ALIGNMENTS

RESULT 1

ID	Q97HW9	PRELIMINARY;	PRT;	107 AA.
AC	Q97HW9;			
DC	01-OCT-2001 (TrEMBLrel. 18, Created)			
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)			
DE	01-OCT-2001 (TrEMBLrel. 18, Last annotation update)			
DE	HFPOTHEICAL PROTEIN CAC1887.			
GN	CAC1887.			
OS	Clostridium acetobutylicum.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;			
OC	Clostridium.			
OX	NCBI_TaxID=1488;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ATCC 824 / DSM 792 / VKM B-1787;			
RX	MEDLINE=21359325; PubMed=11466286;			
RA	Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,			
RA	Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,			
RA	Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,			
RA	Bennett G.N., Koonin E.V., Smith D.R.;			
RT	"Genome sequence and comparative analysis of the solvent-producing			
RT	Bacterium Clostridium acetobutylicum.";			
RL	J. Bacteriol. 183:4823-4838(2001).			
DR	EMBL; AE007697; AAK79851.1;			
RW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 107 AA; 12489 MW; 3DE26914B72DF0F1 CKC64;			

Query Match 3.6%; Score 7; DB 16; Length 107;

Best Local Similarity 100.0%; Pred. No. 20; Mismatches 0; Gaps 0;

Matches 7; Conservative 0;

Qy 20 EKEYEP 26

Db 83 EKEYEP 89

RESULT 2

```

Q96YM2
ID Q96YM2 PRELIMINARY; PRT; 150 AA.
AC Q96YM2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN.
GN ST2152.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Gshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000989; BAB67255.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 150 AA; 17433 MW; 5262C811B145D43B CRC64;

Query Match 3.6%; Score 7; DB 17; Length 150;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 QKEYEYE 25
DB 121 QKEYEYE 127

RESULT 3
Q9HWU2
ID Q9HWU2 PRELIMINARY; PRT; 189 AA.
AC Q9HWU2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PROBABLE PILIN.
GN PA4086.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004825; AAG07473.1; -.
KW Complete proteome.
SQ SEQUENCE 189 AA; 19718 MW; B76DED0410BD4308 CRC64;

Query Match 3.6%; Score 7; DB 16; Length 189;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 168 GLVEAAP 174
DB 142 GLVEAAP 148

RESULT 4
Q93J78
ID Q93J78 PRELIMINARY; PRT; 204 AA.
AC Q93J78;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 21.7 KDA PROTEIN.
GN SCBAC17F8.10C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA O'Neil S., Harris D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL596030; CAC44282.1; -.
KW Hypothetical protein.
SQ SEQUENCE 204 AA; 21680 MW; DC2C849468F88AA4 CRC64;

Query Match 3.6%; Score 7; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 AAPGTAQ 178
DB 90 AAPGTAQ 96

RESULT 5
Q9H611
ID Q9H611 PRELIMINARY; PRT; 266 AA.
AC Q9H611;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CDNA: FL222692 FIS, CLONE HS111184.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isoigai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026345; BAB15456.1; -.
SQ SEQUENCE 266 AA; 28907 MW; 0A291FB7E1339D56 CRC64;

```

Query Match 3.6%; Score 7; DB 4; Length 266;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LLSDCPP 123
 Db 104 LLSDCPP 110
 |||||

RESULT 6
 Q9S0N6 PRELIMINARY; PRT; 283 AA.
 ID Q9S0N6;
 AC Q9S0N6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE C5-O-METHYLTRANSFERASE.
 GN AVED.
 OS Streptomyces avermitilis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=9380548; PubMed=10449723;
 RA Ikeda H., Nonomiya T., Usami M., Ohta T., Omura S.;
 RT "Organization of the biosynthetic gene cluster for the polyketide
 RT anelminthic macrolide avermectin in Streptomyces avermitilis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:9509-9514 (1999).
 DR EMBL; AB032524; BAA84602.1; -.
 DR InterPro; IPR001601; Meth-transf.
 DR InterPro; IPR000051; SAM_bind.
 DR InterPro; IPR004033; ubiE.CO05_methyltransf.
 DR Pfam; PF01209; ubiE_methyltran; 1.
 DR Transferase; Methyltransferase.
 KW TRANSFERASE; Methyltransferase.
 SQ SEQUENCE 283 AA; 30113 MW; 0676E02AD80BC094 CRC64;

Query Match 3.6%; Score 7; DB 2; Length 283;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 AAWALEC 112
 Db 138 AAWALEC 144
 |||||

RESULT 7
 Q9PUS0 PRELIMINARY; PRT; 302 AA.
 ID Q9PUS0;
 AC Q9PUS0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE DECOY TNF RECEPTOR.
 OS Salvelinus fontinalis (Brook trout) (Brook char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8038;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=20111091; PubMed=10642582;
 RA Bobe J., Goetz F.W.;
 RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
 RT the brook trout (Salvelinus fontinalis) ovary at the completion of
 RT ovulation.";
 RL Biol. Reprod. 62:420-426 (2000).
 DR EMBL; AF156738; AAD56428.1; -.
 DR HSSP; O14763; 1D4V.
 DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 3.6%; Score 7; DB 13; Length 302;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 RCPGTY 40
 Db 38 RCPGTY 44
 |||||

RESULT 8
 Q9GPO4 PRELIMINARY; PRT; 327 AA.
 ID Q9GPO4;
 AC Q9GPO4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE IAG-NUCLEOSIDE HYDROLASE.
 OS Trypanosoma vivax.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5699;
 RN [1]
 SEQUENCE FROM N.A.
 RA Pelle R.;
 RT "Molecular cloning and characterization of Trypanosoma (Duttonella)
 RT vivax inosine-adenosine-guanosine preferring (IAG-) nucleoside
 RT hydrolase homolog.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF311701; AAG38561.2; -.
 DR InterPro; IPR001910; IUNH.
 DR Pfam; PF01156; IUN_nuc_hydro; 1.
 DR ProDom; PD007736; IUNH; 1.
 KW Hydrolase.
 SQ SEQUENCE 327 AA; 36330 MW; 034F9833FF6C2825 CRC64;

Query Match 3.6%; Score 7; DB 5; Length 327;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 CTHCELL 118
 Db 245 CTHCELL 251
 |||||

RESULT 9
 Q9SAD4 PRELIMINARY; PRT; 328 AA.
 ID Q9SAD4;
 AC Q9SAD4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE F3F19.1 PROTEIN.
 GN F3F19.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=CV. COLUMBIA;
 RC Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lenz C.,

RA Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A.,
RA Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
RA Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
RT "Arabidopsis thaliana chromosome 1 BAC F3F19 sequence."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007357; AAC31052.1; -;
DR HSP; O80337; 2GCC.
DR InterPro; IPR001471; AP2-domain.
DR Pfam; PF00847; AP2-domain; 1.
DR PRINTS; PR00367; ETHRSPLENT.
DR ProDom; PD001423; AP2-domain; 1.
DR SMART; SM00380; AP2; 1.
SQ SEQUENCE 328 AA; 36319 MW; 66320534B5FCAE6B CRC64;

Query Match 3.6%; Score 7; DB 10; Length 328;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 SSPSARC 158
Db 132 SSPSARC 138
|||||

RESULT 10
Q12953 PRELIMINARY; PRT; 370 AA.
ID Q12953
AC Q12953
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OXIDOREDUCTASE.
GN HCNMA56.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HIPPOCAMPUS;
RA Gmerek R.E., Medford J.I.;
RT "The complete sequence of a human hippocampus gene (HCMA56) shows
homology to developmental genes from Arabidopsis and Brassica napus."
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U13395; AAA21465.1; -;
SQ SEQUENCE 370 AA; 41521 MW; B2F1C523F3AEAEFF CRC64;

Query Match 3.6%; Score 7; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 PGMFCAA 107
Db 87 PGMFCAA 93
|||||

RESULT 11
Q9DJR1 PRELIMINARY; PRT; 371 AA.
ID Q9DJR1
AC Q9DJR1
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
GN HEL.
OS Citrus tristeza virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PB75;
RA Connor R.K., Hallstones D.L., Barkley P., Zhou C.;
RT "Characterisation of Australian strains of CTV."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ399541; CAC19973.1; -;
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF01443; Viral_helicase1; 1.
FT NON_TER 371 371
SQ SEQUENCE 371 AA; 41728 MW; 0B6861589E74684A CRC64;

Query Match 3.6%; Score 7; DB 12; Length 371;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 YEPQHRI 30
Db 128 YEPQHRI 134
|||||

RESULT 12
Q9FR11 PRELIMINARY; PRT; 391 AA.
ID Q9FR11
AC Q9FR11
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PYRUVATE DEHYDROGENASE (FRAGMENT).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SEGUE;
RA Lee H.S., Kim I.J., Chung W.I.;
RT "Isolation of cDNA encoding tomato pyruvate dehydrogenase."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209924; AAG43499.1; -;
DR InterPro; IPR001017; EL_dh.
DR Pfam; PF00676; EL_dehydrog; 1.
FT NON_TER 391 391
SQ SEQUENCE 391 AA; 43373 MW; 4ECDBF97E9DD7F46 CRC64;

Query Match 3.6%; Score 7; DB 10; Length 391;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TEAELKD 131
Db 332 TEAELKD 338
|||||

RESULT 13
Q52181 PRELIMINARY; PRT; 392 AA.
ID Q52181
AC Q52181
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ORF 1.
OS Synechocystis sp. (strain PCC 6803).
OG plasmid pCB2.4.
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;

```

RN  [1]
RC  SEQUENCE FROM N.A.
RP  STRAIN=PCC 6803;
RX  MEDLINE=94302133; PubMed=8029321;
RA  Yang X., McFadden B.A.;
RT  "The complete DNA sequence and replication analysis of the plasmid
RT  pCB2.4 from the cyanobacterium Synechocystis PCC 6803.";
RL  Plasmid 31:131-137(1994).
DR  EMBL; L25424; AAA97418.1; -.
DR  InterPro; IPR003015; HLH_Myc.
KW  PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ  SEQUENCE 392 AA; 42976 MW; 2C0FE7A1A8FECB8D CRC64;

Query Match 3.6%; Score 7; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 EAEKDE 132
    |||||
Db 238 EAEKDE 244

RESULT 14
Q92RW6 PRELIMINARY; PRT; 412 AA.
AC Q92RW6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE PUTATIVE FAD-DEPENDENT OXIDOREDUCTASE PROTEIN.
GN SMC00779.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Guzy J., Gurjel M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorhoelster F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti.";
RL Science 293:668-672(2001).
DR EMBL; AL591784; CAC45296.1; -.
KW Complete proteome.
SQ SEQUENCE 412 AA; 45563 MW; 50456831F27D238E CRC64;

Query Match 3.6%; Score 7; DB 16; Length 412;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 PGTEAEL 129
    |||||
Db 26 PGTEAEL 32

RESULT 15
Q97CE9 PRELIMINARY; PRT; 432 AA.
ID Q97CE9
AC Q97CE9;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

```

```

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TVG0161955 PROTEIN.
GN TVG0161955.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmataceae;
OC Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000991; BA859294.1; -.
DR InterPro; IPR002293; AA_rel_permease_1.
KW Complete proteome.
SQ SEQUENCE 432 AA; 46443 MW; 40D0C6FB1C84D286 CRC64;

Query Match 3.6%; Score 7; DB 17; Length 432;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GTVYSAK 44
    |||||
Db 138 GTVYSAK 144

Search completed: October 4, 2002, 10:20:32
Job time: 235 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2002, 10:10:57 ; Search time 30.1 Seconds
(without alignments)
726.961 Million cell updates/sec

Title: US-09-299-139A-1
Perfect score: 1133
Sequence: 1 SQQAVPPVASENQTCRQDE.....QSDTTCKNPLELPPEMSGT 197

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1133	100.0	197	18 AAW23220	Extracellular doma
2	1133	100.0	197	20 AAV31326	Human lymphotoxin
3	771	68.0	415	22 AAB36700	Human tumour necro
4	456	40.2	77	20 AAW94642	TNF-R extracellular
5	456	40.2	77	22 AAB69194	Human TNF-R extrac
6	315	27.8	518	15 AAR51003	Sequence of a reco
7	309	27.3	461	16 AAR72504	p75 Tumour Necrosi
8	305	26.9	225	21 AAV77463	Primate protein se
9	305	26.9	227	22 AAB66981	Tnfr2 protein. Un
10	305	26.9	235	19 AAW59665	Human soluble tumo
11	305	26.9	235	19 AAW52270	Tumour necrosis fa

12	305	26.9	235	20 AAW89234	Tumour necrosis in
13	305	26.9	235	21 AAY54440	Amino acid sequenc
14	305	26.9	235	21 AAY54443	Wild type N-termna
15	305	26.9	235	22 AAB37685	Human 40 kDa TNF i
16	305	26.9	248	21 AAY94718	Human type 2 tumou
17	305	26.9	461	12 AAR11001	40kD TNF inhibitor
18	305	26.9	461	12 AAR11141	Fusion protein TNF
19	305	26.9	461	14 AAR42058	Fibroblast derived
20	305	26.9	461	21 AAB37801	Human tumour necro
21	305	26.9	461	21 AAB18717	A human tumour nec
22	305	26.9	461	21 AAB01342	Death receptor. H
23	305	26.9	461	22 AAB35331	Human TNF receptor
24	305	26.9	461	22 AAB36698	Human tumour necro
25	305	26.9	461	22 AAB37686	Human 40 kDa TNF i
26	305	26.9	485	13 AAR24016	Fusion protein TNF
27	305	26.9	518	22 AAB70001	TNFR(075):Fc fusi
28	305	26.9	518	22 AAB50080	TNFR:Fc fusion pro
29	304	26.8	235	21 AAY54441	Amino acid sequenc
30	304	26.8	235	21 AAY54442	A K108R/K120R muta
31	303	26.7	183	16 AAR77421	BamTP delta53 nerv
32	295.5	26.1	278	21 AAY95322	Pig costimulatory
33	295	26.0	227	21 AAY77462	Rodent protein seq
34	294	25.9	198	21 AAY94720	Human type 2 tumou
35	290.5	25.6	258	22 AAB50082	Rat TNFR (p80) ext
36	290.5	25.6	487	22 AAB50084	TNFR:Fc fusion pro
37	290	25.6	474	12 AAR11142	TNF-R deduced from
38	289.5	25.6	163	21 AAY94712	Tumour necrosis fa
39	289.5	25.6	165	21 AAB00014	Peptide fragment o
40	289.5	25.6	271	21 AAB19706	Protease-resistant
41	289.5	25.6	271	21 AAB19707	Anino acid sequenc
42	289.5	25.6	271	22 AAB68046	Human mFLINT #2 pr
43	286.5	25.3	273	20 AAY42185	Human FAS ligand i
44	286.5	25.3	300	21 AAB19710	Human FLINT. Homo
45	286.5	25.3	300	21 AAY96597	

ALIGNMENTS

RESULT 1
AAW23220
ID AAW23220 standard; protein; 197 AA.
XX
AC AAW23220;
XX
DT 29-OCT-1997 (first entry)
XX
DE Extracellular domain of human lymphotoxin beta receptor.
XX
KW Human; lymphotoxin beta; receptor; blocking agent; extracellular;
KW ligand binding; domain; treatment; Th1 cell; immune response;
KW delayed; hypersensitivity; contact; tuberculin; granulomatous;
KW graft versus host; disease; organ rejection; autoimmune; disorder;
KW multiple sclerosis; insulin dependent diabetes; uveitis; cytokine;
KW sympathetic ophthalmia; psoriasis; lysteria; toxoplasma; infection;
KW Mycobacterium; abnormal; lymphoid organ; development.
XX
OS Homo sapiens.
XX
PN WO9703687-A1.
XX
PD 06-FEB-1997.
XX
PF 19-JUL-1996; 96WO-US12010.
XX
PR 21-JUL-1995; 95US-0505606.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Benjamin CD, Browning JL, Hochman PS;
XX WPI; 1997-132373/12.
XX

PT Compositions comprising lymphotoxin-beta receptor blocking agent -
PT used to treat auto-immune diseases, e.g. sclerosis,
PT insulin-dependent diabetes, etc.
PS Example 1; Pages 55-56; 76pp; English.
XX
CC The present sequence, a human lymphotoxin beta receptor (LT-beta-R)
CC blocking agent, comprises the extracellular ligand binding domain
CC of the human LT-beta-R up to the transmembrane region. It can be
CC used to treat a Th1 cell mediated immune response which contributes
CC to a delayed type hypersensitivity reaction, preferably contact,
CC tuberculin type or granulomatous hypersensitivity, graft versus
CC host disease, organ rejection or an autoimmune disorder, i.e.
CC multiple sclerosis, insulin dependent diabetes, sympathetic
CC ophthalmia, uveitis and psoriasis. It can also be used to treat
CC conditions exacerbated by the activities of Th-1 type cytokines, or
CC selectively or partially block the LT-beta-R pathway. Its ability to
CC in the treatment of abnormal lymphoid organ development associated
CC with misexpression or overexpression of signalling by the LT-beta-R
CC pathway. The present LT-beta-R blocking agent is capable of
CC selectively inhibiting Th1, but not Th2 cell dependent immune
CC effector mechanisms. As Th1 cytokines can inhibit Th2 cell
CC dependent responses, the present LT-beta-R blocking agent may also
CC indirectly stimulate certain Th2 cell dependent responses which are
CC normally inhibited by Th1 induced cytokines. Doses of about 1 mg/kg
CC of the present soluble LT-beta-R are expected to be suitable
CC starting doses for optimising treatment.
XX
XX Sequence 197 AA;
SQ
Query Match 100.0%; Score 1133; DB 18; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.7e-84;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQQAVPPVASENQTRDQEKVEYEPQHRICCSRCPPGTYVSAKSRIRDTVCATCAENS 60
Db 1 sgpqavppvasenqtrcdqekveyepqhriccsrccppgtyvsaksrirdtvcatacens 60
QY 61 YNEHWNLTICOLCRPCDPVGMGLEETAPCTSKRKTQCRQPGMFCAAWALECTHCELLSD 120
Db 61 ynehwnlyticqlcrpcdpvmgleelapctskrktqrcqpgmfcaawalecthcelsd 120
QY 121 CPPGTEAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAGTAQSD 180
Db 121 cpgpteaelkdevgknnhcvpcckaghfntsspsarcqphtrcenqglveaapgtagsd 180
QY 181 TTCKNPLELPPEMSGT 197
Db 181 ttcknplelppemsgt 197
RESULT 2
ID AAY31326
XX AAY31326 standard; peptide; 197 AA.
AC AAY31326;
XX
XX 04-OCT-1999 (first entry)
XX Human lymphotoxin (LT)beta-receptor extracellular region.
XX
XX Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;
KW immune system; tumour; follicular lymphoma; extracellular domain; human.
XX
XX Homo sapiens.
OS WO938525-A1.
XX
XX 05-AUG-1999.
PD
XX 29-JAN-1999; 99WO-US01928.
PF

XX 02-FEB-1998; 98US-0073410.
PR 30-JAN-1998; 98US-0073112.
XX
PA (BIOJ) BIOGEN INC.
XX
XX Browning J, Thorbecke J, Tsiagbe V;
XX WPI; 1999-469242/39.
XX New method of treating follicular lymphomas by inhibiting
PT interaction between lymphotoxin-beta and its receptor
XX
XX Example 1; Page 25-26; 31pp; English.
XX The invention provides a method for arresting or reducing, severity of
CC effects of a tumour by administration of a composition which inhibits
CC the interaction between lymphotoxin (LT)-beta and its receptor. An
CC inhibitor of the interaction between LT-beta and its receptor can be
CC administered for the survival or maintenance of follicular
CC dendritic cells in a subject and for altering the architecture of the
CC organs of the immune system. The method is useful for treating tumours,
CC specifically follicular lymphomas. It offers an alternative therapy for
CC those with tumours resistant to traditional chemotherapy. The present
CC sequence represents the extracellular region of the human Lfbeta-receptor
CC and comprises the ligand binding domain.
XX
XX Sequence 197 AA;
SQ
Query Match 100.0%; Score 1133; DB 20; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.7e-84;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQQAVPPVASENQTRDQEKVEYEPQHRICCSRCPPGTYVSAKSRIRDTVCATCAENS 60
Db 1 sgpqavppvasenqtrcdqekveyepqhriccsrccppgtyvsaksrirdtvcatacens 60
QY 61 YNEHWNLTICOLCRPCDPVGMGLEETAPCTSKRKTQCRQPGMFCAAWALECTHCELLSD 120
Db 61 ynehwnlyticqlcrpcdpvmgleelapctskrktqrcqpgmfcaawalecthcelsd 120
QY 121 CPPGTEAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAGTAQSD 180
Db 121 cpgpteaelkdevgknnhcvpcckaghfntsspsarcqphtrcenqglveaapgtagsd 180
QY 181 TTCKNPLELPPEMSGT 197
Db 181 ttcknplelppemsgt 197
RESULT 3
ID AAB36700 standard; Protein; 415 AA.
XX
XX AAB36700;
XX
XX 15-MAR-2001 (first entry)
XX Human tumour necrosis factor receptor LfbR protein SEQ ID NO:6.
XX
XX Human; tumour necrosis factor receptor 5; TR5; TR5; nontropic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotrophic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
XX Homo sapiens.
OS
XX WO200071150-A1.
PN

XX PD 30-NOV-2000.
 XX XX
 XX PF 18-MAY-2000; 2000WO-US13515.
 XX XX
 XX PR 20-MAY-1999; 99US-0135164.
 XX XX
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX XX
 XX PI Wei Y, Ruben SM, Gentz RL, Ni J;
 XX XX
 XX DR WPI; 2001-041051/05.
 XX XX
 XX PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor
 XX PT necrosis factor receptor 5, useful in the diagnosis, treatment or
 XX PT prevention of cancer, autoimmune disorders and viral infection -
 XX XX
 XX PS Disclosure; Fig 2; 285pp; English.
 XX XX
 XX CC The present invention describes the human TRID protein (tumor necrosis
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
 CC intracellular domain, also referred to as tumor necrosis factor
 CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
 CC nototropic, neuroprotective, antiviral, antiparkinsonian and vasotropic
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
 CC activities, and can be used in gene therapy. The TRID polynucleotides
 CC are useful for detecting complementary polynucleotides. TRID proteins and
 CC polynucleotides are useful in the treatment of tumours, resistance to
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.
 CC They are also useful for inducing proliferation of T-cells, endothelial
 CC cells and certain haematopoietic cells, to regulate antiviral responses
 CC and to prevent certain autoimmune diseases after stimulation of TRID by
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
 CC polypeptides are useful for treating and/or preventing diseases
 CC associated with increased or decreased apoptotic cell death. The TRID
 CC polynucleotides, proteins, antibodies, agonists and antagonists are
 CC useful in the diagnosis, treatment or prevention of: (a) cancer;
 CC (b) autoimmune disorders; (c) diseases associated with increased
 CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
 CC present sequence represents a tumor necrosis factor receptor used in
 CC comparison with TRID in the exemplification of the present invention.
 XX XX
 XX SQ Sequence 415 AA;
 Query Match 68.0%; Score 771; DB 22; Length 415;
 Best Local Similarity 70.7%; Pred. No. 2.1e-54;
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;
 Qy 1 SOPQAVPPYASENQTCDQKEYYEYPOHRIICSCRPCTGYVSARKSIRIDTVCATCAENS 60
 Db 28 sqqlvppyrleqtcdwqdkqeyypmhdvccstpcpggefvcvcsrqdvtcktcphns 87
 Qy 61 YNEHWNLTICQLCRPCDPVVGLEIEIAPCTSKRTQCRQCGMFCAAWALECTHC--ELL 118
 Db 88 ynehnwlnstqlcrpcdpdivgfveevapctsdkaecrcpgmscvyldncvchceerl 147
 Qy 119 SDCPPGTEAEKLGKGVGNHCVCPKAGHFQNTSSPSARCPQPHTRCENQGLVEAAGPQAQ 178
 Db 148 vlcpqgtaeavtdelmdtdncvpcpkpghfntssprarcqphtrcqlqglveaapgtsty 207
 Qy 179 SDTTCNPNLEP 189
 Db 208 sdticknppep 218
 RESULT 4
 AAW94642
 ID AAW94642 standard; peptide; 77 AA.
 XX AC
 XX AC AAW94642;
 XX DT 29-APR-1999 (first entry)

XX DE TNF-R extracellular Cys-rich domain TNF-R-rp.
 XX KW
 KW Tumour necrosis factor receptor; TNF-R; autoimmune diseases;
 KW inflammation; septic shock; cachexia; graft versus host disease;
 KW skin allergic reaction; immune complex disease; malaria;
 KW transplantation rejection.
 XX OS Homo sapiens.
 XX XX
 XX PN WO9853842-A1.
 XX XX
 XX PD 03-DEC-1998.
 XX XX
 XX PF 29-MAY-1998; 98WO-US10891.
 XX XX
 XX PR 30-MAY-1997; 97US-0866545.
 XX XX
 XX PA (UYPE-) UNIV PENNSYLVANIA.
 XX XX
 XX PI Greene MI, Murali R, Takasaki W;
 XX XX
 XX DR WPI; 1999-080781/07.
 XX XX
 XX PT New compounds designed from a binding loop of a tumour necrosis
 XX PT factor receptor - are capable of inhibiting the biological
 XX PT activities of tumour necrosis factor, e.g., in treating inflammation
 XX PT or autoimmune diseases
 XX XX
 XX PS Disclosure; Fig 1; 78pp; English.
 XX XX
 XX CC The present invention describes peptides and peptide analogues which
 CC correspond in primary sequence to a binding loop of a tumour necrosis
 CC factor receptor (TNF-R) superfamily member. The compounds are especially
 CC designed from a binding loop of TNF-R p55. They are capable of
 CC inhibiting TNF binding to its cellular receptors and may be used to
 CC inhibit the biological activities of TNF. They may be used in treating
 CC TNF-associated conditions such as acute and chronic inflammatory
 CC responses, septic shock, cachexia, autoimmunity, graft-versus-host
 CC disease, skin allergic reactions, immune complex disease,
 CC transplantation rejection and malaria. Administration is, e.g. oral,
 CC transdermal, transmucosal, pulmonary, subcutaneous, intravenous or
 CC intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present
 CC sequence represents an extracellular Cys-rich domain of TNF-R from the
 CC present invention.
 XX XX
 XX SQ Sequence 77 AA;
 Query Match 40.2%; Score 456; DB 20; Length 77;
 Best Local Similarity 100.0%; Pred. No. 9.2e-30;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 52 VCATCAENSYNHWNLTICQLCRPCDPVVGLEIEIAPCTSKRTQCRQCGMFCAAWALE 111
 Db 1 vcatcaensynhwnlticqlcrpcdpvvgmgleieiapctskrtqcrqpgmfcawale 60
 Qy 112 CTHCELLSDCPPGTEAE 128
 Db 61 cthcellsdcpptgeae 77
 RESULT 5
 AAB69194
 ID AAB69194 standard; protein; 77 AA.
 XX AC
 XX AC AAB69194;
 XX DT 30-APR-2001 (first entry)
 XX DE Human TNF-R extracellular Cys-rich domain TNF-R-rp SEQ ID NO:3.
 XX KW Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;

KW osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic;
KW antirheumatic; antiarthritic; antiinflammatory; immunomodulatory;
KW tumour necrosis factor-related activation-induced cytokine; TRANCE;
KW receptor activator of NF-kappaB ligand; RANK; osteoporosis;
KW Paget's disease; metastatic bone disease; rheumatoid arthritis;
KW periodontal disease; modulating dendritic cell maturation;
KW T cell proliferation; CD40 receptor system.
XX
OS Homo sapiens.
XX
XX WO200108699-A1.
PN
XX 08-FEB-2001.
XX
XX 28-JUL-2000; 2000WO-US20510.
PF
XX 28-JUL-1999; 99US-0146090.
PR
XX (UYPE-) UNIV PENNSYLVANIA.
PA (AOKI/) AOKI K.
PA (HORN/) HORNE W C.
PA (BARO/) BARON R.
XX
XX Aoki K, Horne WC, Baron R, Greene MI, Murali R;
PI
XX WPI; 2001-182866/18.
DR
XX
XX use of peptides and peptide analogs which are TRANCE/RANK inhibitors,
PT for inhibiting osteoclastogenesis and bone resorption
PT
XX Disclosure; Fig 1; 81pp; English.
PS
XX The present invention describes a method for inhibiting
CC osteoclastogenesis and bone resorption. Osteoclastogenesis and bone
CC resorption inhibiting peptide analogues from the present invention have
CC osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory
CC and immunomodulatory activities, and are tumour necrosis factor (TNF)-
CC related activation-induced cytokine (TRANCE)/receptor activator of
CC NF-kappaB ligand (RANK) inhibitors. The method is useful for treating
CC diseases characterised by bone loss such as osteoporosis, Paget's
CC disease, metastatic bone disease, rheumatoid arthritis or periodontal
CC disease, and modulating dendritic cell maturation, T cell proliferation,
CC and/or CD40 receptor systems. The present sequence represents an
CC extracellular Cys-rich domain of a tumour necrosis factor receptor
CC (TNF-R) superfamily member, which is used in the exemplification of
CC the present invention.
XX
XX Sequence 77 AA;
SQ
Query Match 40.2%; Score 456; DB 22; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.2e-30;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 VCATCAENSYNHWNLYTICQLCRPCDPVWGLEETAPCTSRKRTQCRQPGMFCFAAWALE 111
Db 1 vcatcaensynhwnlyticqlcrpcdpvwmgleetapctsrkrtqcrpgmfcfaawale 60
QY 112 CTHCELLSDCPPTGAE 128
Db 61 cthcellsdcppgtea 77
RESULT 6
AAR51003
ID AAR51003 standard; Protein; 518 AA.
AC AAR51003;
XX
XX 07-OCT-1994 (first entry)
DT
XX Sequence of a recombinant human (rhu) tumour necrosis factor receptor
DE TNFR/fc fusion protein.

XX Tumour necrosis factor receptor; chimeric antibody molecule;
KW immunoglobulin.
XX
OS Synthetic.
XX WO9406476-A.
PN
XX 31-MAR-1994.
PD
XX 14-SEP-1993; 93WO-US08666.
PF
XX 15-SEP-1992; 92US-0946236.
PR
XX (IMMV) IMMUNEX CORP.
PA
PI Jacobs CA, Smith CA;
XX
XX WPI; 1994-118172/14.
DR N-PSDB; AAQ45225.
DR
XX Treating TNF mediated inflammatory diseases with TNF antagonist -
PT esp. soluble form of TNF receptor, opt. as fusion protein with
PT human immunoglobulin Fc region, esp. for treating arthritis
PT
XX Disclosure; Page 32-34; 47pp; English.
PS
XX AAQ45224 is cDNA from clone 1 of library WI-26 V44 of human fibroblast
CC cell line WI-26 V44. The mature full-length TNFRI is a glycoprotein
CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
CC TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1
CC is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A
CC recombinant chimeric antibody may be produced having TNFR sequences
CC substituted for the variable domains of either or both of the
CC immunoglobulin molecule heavy and light chains and having
CC unmodified constant region domains. A specific example of a TNFR/Fc
CC fusion protein is given in AAQ45225/R51003. The rhu TNFR/Fc fusion
CC gene was created by ligating the following fragments into a cloning
CC vector: 1) an 867 bp Asp718-Pvu2 fragment from pCAV/NOT-TNFR (ATCC
CC 68088) contg. the cDNA encoding the truncated TNFR. 2) a 700 bp
CC Styl-Spel fragment from plasmid pIXY498 coding for 232 AAs of the
CC Fc portion of human IgG1. Plasmid pIXY498 is a yeast expression
CC vector contg. the Fc fragment of human IgG1. 3) An oligo linker, to
CC fuse the truncated TNFR with the human IgG1 Fc fragment. This
CC linker was created by PCR using primer AAQ45226, which encodes the 3'-
CC end of the truncated TNF receptor and the 5' end of human IgG1,
CC and primer AAQ45227, which is an antisense sequence encoding bps
CC 257-237 of human IgG1.
XX
XX Sequence 518 AA;
SQ
Query Match 27.8%; Score 315; DB 15; Length 518;
Best Local Similarity 35.5%; Pred. No. 1.5e-17;
Matches 71; Conservative 24; Mismatches 77; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTCRQDEKEYEPQHRICSRCPGPGTYYSAKCSRINDTVCAATCAENSYN 63
Db 57 aftpyapepgstcr--lreydydqtqmcscskspgqhakvftctsdtdcdscdstytq 114
QY 64 HNNYLTICQLCR---PCDPVWGLEETAPCTSRKRTQCRQPGMFCFAAWALE-CTHCELLS 119
Db 115 lwnvpeclscgrscsdqv----etqactreqnrictrcpwycalskqegcricalpr 170
QY 120 DCPPG-----FEALKDEVGKGNHCVCKAGHFONTSSPSARCOPHTRCENQGVAAAP 174
Db 171 kcrpfgvarpgtetsdvv-----ckpapgftntstsdicrphqicn-----vvaip 220
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 221 gnasmdavctststsrmap 240

```
RESULT 7
AAR72504
ID AAR72504 standard; Protein; 461 AA.
XX AC AAR72504;
XX DT 31-OCT-1995 (first entry)
XX AC AAR72504;
XX DE p75 Tumour Necrosis Factor Receptor.
XX KW Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
XX KW receptor.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Region 27..214
XX FT /label= TPPII.
XX FT Domain 258..285
XX FT /label= Transmembrane domain.
XX FT Misc-difference 259
XX FT /note= "Unidentified amino acid."
XX PN EP648783-A.
XX PD 19-APR-1995.
XX PF 11-OCT-1994; 94EP-0116015.
XX PR 12-OCT-1993; 93IL-0107267.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PA (WALL/) WALLACH D.
XX PI Beletsky I, Bigda J, Mett I, Wallach D;
XX WPI: 1995-148673/20.
XX DR N-PSDB: AAQ89544.
XX PT Tumour necrosis factor (TNF) receptor ligand - used to increase
XX PT inhibitory effect of a soluble TNF receptor
XX PS Disclosure; Figure 2; 18pp; English.
XX CC A ligand to a member of the tumour necrosis factor (TNF)/nerve
XX CC growth factor (NGF) receptor family which binds either to the region
XX CC of the 4th-Cys rich domain of the receptor, or to the region between
XX CC it and the cell membrane may be used in the production of a
XX CC pharmaceutical composition for increasing the inhibitory effect of a
XX CC soluble receptor of the TNF/NGF receptor family. This sequence
XX CC is the sequence of the p75 TNF receptor.
XX SQ Sequence 461 AA;

Query Match 27.3%; Score 309; DB 16; Length 461;
Best Local Similarity 35.5%; Pred. No. 4e-17;
Matches 71; Conservative 24; Mismatches 77; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTCRQKEYYEPOHRTCCSRCPGCTVVSACSKSRIRTVCAENSYNE 63
| ||| | ||| :|||: ||| : ||| : ||| : ||| : ||| :
Db 28 aftypapepgstor--lreydydtaqmcscskspgghakafctktsdtdvcdscdstytq 85
| ||| | ||| :|||: ||| : ||| : ||| : ||| : ||| :
QY 64 HWNYLTTCQLCR---PCDPVWGLGEIAPCTSKRTQCRQCPGMECAWALE-CTHCELLS 119
| ||| | ||| :|||: ||| : ||| : ||| : ||| : ||| :
Db 86 lwnwpeclscgscrsdqv----etqactreqrictcrpgwycalskqegcrlcaplr 141
| ||| | ||| :|||: ||| : ||| : ||| : ||| : ||| :
QY 120 DCPPG-----TEAEIKDEVGKGNHNVPCRKAGHPQNTSSPSARQCPHTRCNQGLVEAAP 174
| ||| | ||| :|||: ||| : ||| : ||| : ||| : ||| :
Db 142 kcrpgfgvargptgtsdvv-----ckpcapgtfisttsdtdcrphqicn----vvaip 191
| ||| | ||| :|||: ||| : ||| : ||| : ||| : ||| :
QY 175 GTAQSDTTC--KNPLEPLPP 192
| ||| | ||| :|||: ||| : ||| : ||| : ||| : ||| :
```

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Db 192 gnasmdavctstptsmap 211
RESULT 8
AAY77463
ID AAY77463 standard; Protein; 225 AA.
XX AC AAY77463;
XX DT 05-JUN-2000 (first entry)
XX AC AAY77463;
XX DE Primate protein sequence, SEQ ID NO:14.
XX KW Immune disorder; inflammation; allergy; immunosuppressant;
XX KW antiarthritic; antirheumatoid; antiinflammatory; dermatological;
XX KW antithyroid.
XX OS Primates.
XX PN WO200001817-A2.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-US12366.
XX PR 06-JUL-1998; 98US-0110938.
XX PR 13-JUL-1998; 98US-0114466.
XX PR 23-JUL-1998; 98US-0093897.
XX PR 12-AUG-1998; 98US-0132968.
XX PR 18-AUG-1998; 98US-0136214.
XX PR 11-SEP-1998; 98US-00999999.
XX PA (SCHE ) SCHERING CORP.
XX PI Bates EEM, Lebecque SJE, Murphy EE, Mattson JD, Gorman DM;
XX PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
XX PI Bazan JF, Mahony D, Lees EM;
XX WPI: 2000-171015/15.
XX PT New isolated mammalian genes, used to develop products for treating
XX PT e.g. immune, inflammatory or allergic abnormalities, cancers or
XX PT degenerative conditions
XX PS Disclosure; Page 170-171; 218pp; English.
XX CC The invention relates to a number of primate and/or rodent proteins, and
XX CC the genes which encode them. The invention encompasses human dendritic
XX CC cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis
XX CC factor) receptor family-related proteins HDTEA84, HSLJD37R and RANKL;
XX CC human CC chemokine HCC5; human deubiquitinating proteins Dub1 and Dub
XX CC 12; human MD-1 and human and murine MD-2 proteins, which exhibit the
XX CC properties of ligands for proteins comprising a leucine-rich motif
XX CC (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies
XX CC against these proteins. The proteins can be used for modulating the
XX CC physiology or development of a cell. They can be used to mediate uptake
XX CC of substrates (e.g., prostaglandin-like molecules), to modulate or
XX CC mediate cellular interactions (e.g., induce or prevent trafficking,
XX CC proliferation, or differentiation of cells), or are intracellular
XX CC proteins which are important in various cellular processes such as the
XX CC deubiquitination of proteins or cell cycle regulation. The products can
XX CC be used for treating medical conditions such as immune, inflammatory or
XX CC allergic disorders, or abnormal cellular proliferation, for example,
XX CC cancers or degenerative conditions. They can be used to modulate immune
XX CC responses in disease states e.g., autoimmune disorders, including
XX CC rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's
XX CC autoimmune thyroiditis, as well as acute and chronic inflammatory
XX CC responses in which T cell activation, expansion, and/or immunological T
XX CC cell memory play an important role. Sequences AAY77463-Y77464,
XX CC AAY77474-Y77475 and AAY77484 represent primate proteins of undefined
XX CC function, AAY77462 and AAY77481 are rodent proteins of undefined
XX CC function, and AAY77482 is an avian protein of undefined function. These
XX CC sequences are given in the sequence listing but are not referred to in
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CC the remainder of the specification.

XX Sequence 225 AA;

SQ Query Match 26.9%; Score 305; DB 21; Length 225;

Best Local Similarity 35.0%; Pred. No. 4e-17;

Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPVASE-NQTCRQOEKEYEPOHRIICSCRCPPGTYIVSAKSRIDTVCAATCAENSYNE 63

DB 28 aftypapepgstcr--lreyydtqagmccskspgghakvftcktsdtvcdscdestyq 85

QY 64 HNNYLTICQLCR---PCDPVVMGLEIAPCTSKRKTCRCQCPGMFCAAWALE-CTHCELLS 119

DB 86 lwnvpeclscgscrsdq-----etqactreqntrictorpgwycalskqegcricaplr 141

QY 120 DCPPG-----TEAEKDEYKGNHCVCKAGHFONTSPSARCOPHRCENQGLVEAAP 174

DB 142 kcrpgfgvarpgtetsdv-----ckpcapgtfnttsdtdicrphqicn----vvaip 191

QY 175 GTAQSDTTC--KNPLEPLPP 192

DB 192 gnasmдавtсtсptrsmap 211

RESULT 9

AAB66981

ID AAB66981 standard; Protein; 227 AA.

AC AAB66981;

DT 19-APR-2001 (first entry)

DE Tnfr2 protein.

XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;

XX multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;

XX systemic lupus erythematosus; graft-versus-host disease; septic shock;

XX acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;

XX coronary condition; myocardial infarction; cancer; diabetes; psoriasis;

XX endometriosis; fever; glomerulonephritis; inflammatory bowel disease;

XX ischaemia; Parkinson's disease.

XX Unidentified.

XX WO200103719-A2.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-US18667.

XX 09-JUL-1999; 99US-0350670.

XX 09-DEC-1999; 99US-0457647.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX WPI; 2001-103031/11.

XX Treating conditions leading to bone loss such as rheumatoid arthritis,

XX multiple sclerosis and asthma, comprises administering an

XX osteoprotegerin protein in conjunction with e.g. inhibitors of

XX interleukin and tumor necrosis factor alpha

XX Disclosure; Fig 2; 316pp; English.

XX The present invention relates to a method for treating conditions leading

XX to bone loss. The method comprises administering a purified and isolated

XX osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)

XX in conjunction with other substances such as tumor necrosis factor-alpha

XX (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE

CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet

CC activating factor (PAF) antagonists. The method is useful for treating

CC conditions leading to bone loss such as rheumatoid arthritis, multiple

CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also

CC useful for treating inflammation, systemic lupus erythematosus (SLE) and

CC graft-versus-host disease (GVHD). Other diseases that can be treated

CC include acute pancreatitis, Alzheimer's disease, anorexia,

CC atherosclerosis, coronary conditions (e.g. myocardial infarction),

CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,

CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,

CC psoriasis and septic shock. The present sequence was used in a sequence

XX homology comparison.

SQ Sequence 227 AA;

Query Match 26.9%; Score 305; DB 22; Length 227;

Best Local Similarity 35.0%; Pred. No. 4.e-17;

Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPVASE-NQTCRQOEKEYEPOHRIICSCRCPPGTYIVSAKSRIDTVCAATCAENSYNE 63

DB 28 aftypapepgstcr--lreyydtqagmccskspgghakvftcktsdtvcdscdestyq 85

QY 64 HNNYLTICQLCR---PCDPVVMGLEIAPCTSKRKTCRCQCPGMFCAAWALE-CTHCELLS 119

DB 86 lwnvpeclscgscrsdq-----etqactreqntrictorpgwycalskqegcricaplr 141

QY 120 DCPPG-----TEAEKDEYKGNHCVCKAGHFONTSPSARCOPHRCENQGLVEAAP 174

DB 142 kcrpgfgvarpgtetsdv-----ckpcapgtfnttsdtdicrphqicn----vvaip 191

QY 175 GTAQSDTTC--KNPLEPLPP 192

DB 192 gnasmдавtсtсptrsmap 211

RESULT 10

AAW59665

ID AAW59665 standard; Protein; 235 AA.

XX AAW59665;

XX 28-SEP-1998 (first entry)

XX Human soluble tumour necrosis factor receptor type II.

XX Human; tumour necrosis factor; TNF; TNF receptor type II;

XX inflammatory disease; leukaemia; TNF binding protein;

XX anti-inflammatory drug; methotrexates.

XX Homo sapiens.

XX WO9824463-A2.

XX 11-JUN-1998.

XX 08-DEC-1997; 97WO-US22733.

XX 09-JUL-1997; 97US-0052023.

XX 06-DEC-1996; 96US-0032587.

XX 23-JAN-1997; 97US-0036355.

XX 07-FEB-1997; 97US-0039315.

XX (AMGE-) AMGEN INC.

XX Bendele AM, Edwards CK, Sennello RM;

XX WPI; 1998-333039/29.

XX N-PSDB; AAV41549.

XX Treatment of acute or chronic inflammatory disease, e.g. leukaemia -

PT by administering tumour necrosis factor binding protein and at least


```

XX New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
XX
XX Disclosure; Fig 3; 92pp; English.
XX
XX The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents the TNF inhibitor 40 kDa
CC protein.
XX Sequence 235 AA;
SQ
Query Match 26.9%; Score 305; DB 20; Length 235;
Best Local Similarity 35.0%; Pred. No. 4.2e-17;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
Qy 5 AVPPYASE-NOTCRDQKEYEYPOHRIICSCRPPTYYVSACSRIRDTVCATCAENSUNE 63
Db 6 aftypaeggstcr--lreydydtaqmccskspqghakvfctkstdvcdscdstyqt 63
Qy 64 HWNYLTICQLCR---PCDPVVMGLEIEIAPCTSKRKTKQCRQPMFCAAWALE-CTHCELLS 119
Db 64 lwnwvpeclscgscscsdqv-----etqactreqnrictrcpwyalskgqegcrlicaplr 119
Qy 120 DCPPG-----TEAEKLDVKGNNHCVPCKAGHFONTSSPSCARCPHTRCENQGLVEAAP 174
Db 120 kcrpgfgvarpgtetsdv-----ckpcapgtfntstsdicrphqlcn----vvaalp 169
Qy 175 GTAQSDTTC--KNPLELPP 192
Db 170 gnasrdavctstsptrsmap 189
RESULT 13
AAY54440
ID AAY54440 standard; Protein; 235 AA.
XX
XX AAY54440;
XX
XX 25-APR-2000 (first entry)
XX
XX Amino acid sequence of a K108R mutant of soluble p75 TNF receptor.
XX
XX p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;
KW polyethylene glycol conjugation; PEG conjugation; protein activity.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 108
FT /note= "wild type Lys replaced with Arg"
XX
XX WO9967291-A2.
XX
XX 29-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US13953.
XX

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XX 22-JUN-1998; 98US-0102530.
XX (IMMV ) IMMUNEX CORP.
XX
XX Pettit DK;
XX
XX WPI; 2000-160577/14.
XX N-PSDB; AAZ45759.
XX
XX Novel methods for site-specific protein modification by mutagenesis by
PT replacing polyethylene glycol reacting sites
XX
XX Claim 17; Page 29; 36pp; English.
XX
XX The present sequence represents a N-terminal fragment of a mutant of
CC the soluble tumour necrosis factor (TNF) receptor, where the wild
CC type Lys residue at position 108 is replaced with Arg. Lys108 (and
CC Lys120) make contact between the p75 receptor and ligand. These
CC residues are also potential polyethylene glycol (PEG) conjugation
CC sites. The wild type p75 TNF receptor protein was mutated and conjugated
CC to PEG, using the method of the invention. The specification describes
CC a method for conjugating proteins with PEG to result in
CC PEG-conjugated proteins having little or no reduction in a desired
CC activity. Specifically, one or more amino acid residues that are
CC critical for protein bioactivity and which are capable of reacting
CC with PEG sites are deleted, prior to conjugation of the protein to PEG.
CC The methods provide PEG conjugated proteins that are more homogeneous
CC and present in higher yields. Conjugation does not take place at amino
CC acid residues that are critical to the proteins bioactivity, thus
CC maintaining the activity of the protein. The methods are used to
CC produce PEG conjugated proteins.
XX Sequence 235 AA;
SQ
Query Match 26.9%; Score 305; DB 21; Length 235;
Best Local Similarity 35.0%; Pred. No. 4.2e-17;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
Qy 5 AVPPYASE-NOTCRDQKEYEYPOHRIICSCRPPTYYVSACSRIRDTVCATCAENSUNE 63
Db 6 aftypaeggstcr--lreydydtaqmccskspqghakvfctkstdvcdscdstyqt 63
Qy 64 HWNYLTICQLCR---PCDPVVMGLEIEIAPCTSKRKTKQCRQPMFCAAWALE-CTHCELLS 119
Db 64 lwnwvpeclscgscscsdqv-----etqactreqnrictrcpwyalskgqegcrlicaplr 119
Qy 120 DCPPG-----TEAEKLDVKGNNHCVPCKAGHFONTSSPSCARCPHTRCENQGLVEAAP 174
Db 120 kcrpgfgvarpgtetsdv-----ckpcapgtfntstsdicrphqlcn----vvaalp 169
Qy 175 GTAQSDTTC--KNPLELPP 192
Db 170 gnasrdavctstsptrsmap 189
RESULT 14
AAY54443
ID AAY54443 standard; Protein; 235 AA.
XX
XX AAY54443;
XX
XX 25-APR-2000 (first entry)
XX
XX Wild type N-terminal fragment of the soluble p75 TNF receptor.
XX
XX p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;
KW polyethylene glycol conjugation; PEG conjugation; protein activity.
XX
XX Homo sapiens.
OS
XX
XX WO9967291-A2.
XX

```


XX 29-DEC-1999.
XX 18-JUN-1999; 99WO-US13953.
XX 22-JUN-1998; 98US-0102530.
XX (IMV) IMMUNEX CORP.
XX Pettit DK;
XX WPI: 2000-160577/14.
XX N-PSDB; AAZ45762.
XX Novel methods for site-specific protein modification by mutagenesis by
XX replacing polyethylene glycol reacting sites -
XX Claim 16; Page 35-36; 36pp; English.
XX
XX The present sequence represents a N-terminal fragment of the soluble
XX tumour necrosis factor (TNF) receptor. The wild type Lys residues at
XX positions 108 and 120 are replaced with Arg (see AAY5441-42). Lys120
XX and Lys108 make contact between the p75 receptor and ligand. These
XX residues are also potential polyethylene glycol (PEG) conjugation
XX sites. The wild type p75 TNF receptor protein was mutated and conjugated
XX to PEG, using the method of the invention. The specification describes
XX a method for conjugating proteins with PEG to result in
XX PEG-conjugated proteins having little or no reduction in a desired
XX activity. Specifically, one or more amino acid residues that are
XX critical for protein bioactivity and which are capable of reacting
XX with PEG sites are deleted, prior to conjugation of the protein to PEG.
XX The methods provide PEG conjugated proteins that are more homogeneous
XX and present in higher yields. Conjugation does not take place at amino
XX acid residues that are critical to the proteins bioactivity, thus
XX maintaining the activity of the protein. The methods are used to
XX produce PEG conjugated proteins.
XX
XX Sequence 235 AA;

Query Match 26.9%; Score 305; DB 21; Length 235;
Best Local Similarity 35.0%; Pred. No. 4.2e-17;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
Qy 5 AVPPYASE-NOTCRDQEKYEYEQHRIICCSRCPPGTYYSAKSRIRDTVCATCAENSYNE 63
Db 6 aftypapepgstcr--lreydydtaqmcscskspgqhakvftktsdtvcdscdstytq 63
Qy 64 HWNYLTICQLCR---PCDPVVMGLEIEIAPCTSKRTQCRQCPGMFCMAWALE-CTHCELLS 119
Db 64 lwnwvpeclscgscrcssdqv---etqactreqnrictcrpgwycalskqegcrlcaplr 119
Qy 120 DCPPG-----TEALKDVGKGNHVCPCAGHFQNTSSPSARCOPHTRCENOGIVEAAP 174
Db 120 kcrpgfgvarpgtstsdv-----ckpapgftsfntstsdicrphqicn-----vvaip 169
Qy 175 GTAQSDTTC--KNPLEPLPP 192
Db 170 gnsmdavctststsrmap 189

RESULT 15
AAB37685
ID AAB37685 standard; Protein; 235 AA.
XX AAB37685;
XX
XX 02-MAR-2001 (first entry)
XX Human 40 kDa TNF inhibitor.
XX
XX TNF inhibitor; antinflammatory; Tumour Necrosis Factor; interleukin;
XX IL-1; inflammatory disease; degenerative disease; human; lymphotoxin.

XX Homo sapiens.
XX US6143866-A.
XX 07-NOV-2000.
XX 19-JAN-1995; 95US-0375242.
XX 19-JUL-1990; 90US-0555274.
XX 08-JUL-1993; 93US-0090366.
XX 18-JUL-1989; 89US-0381080.
XX 11-DEC-1989; 89US-0450329.
XX 07-FEB-1990; 90US-0479661.
XX (AMGE-) AMGEN INC.
XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
XX Vanderslice RW, Vannice J, Kohno T;
XX WPI: 2001-006443/01.
XX Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
XX non-native cysteine residue cross-linked with polyethylene glycol,
XX useful for treating inflammatory and degenerative diseases mediated by
XX TNF -
XX Example 12; Fig 38; 82pp; English.
XX
XX The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
XX (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
XX novel TNF inhibitors of the present invention are useful as therapeutic
XX agents for inhibiting the activity of TNF and interleukin (IL-1), and
XX for treating inflammatory and degenerative diseases mediated by TNF. The
XX present sequence is 40 kDa TNF inhibitor. The 40 kDa TNF inhibitor can
XX inhibit both TNF alpha and beta (lymphotoxin).
XX
XX Sequence 235 AA;

Query Match 26.9%; Score 305; DB 22; Length 235;
Best Local Similarity 35.0%; Pred. No. 4.2e-17;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
Qy 5 AVPPYASE-NOTCRDQEKYEYEQHRIICCSRCPPGTYYSAKSRIRDTVCATCAENSYNE 63
Db 6 aftypapepgstcr--lreydydtaqmcscskspgqhakvftktsdtvcdscdstytq 63
Qy 64 HWNYLTICQLCR---PCDPVVMGLEIEIAPCTSKRTQCRQCPGMFCMAWALE-CTHCELLS 119
Db 64 lwnwvpeclscgscrcssdqv---etqactreqnrictcrpgwycalskqegcrlcaplr 119
Qy 120 DCPPG-----TEALKDVGKGNHVCPCAGHFQNTSSPSARCOPHTRCENOGIVEAAP 174
Db 120 kcrpgfgvarpgtstsdv-----ckpapgftsfntstsdicrphqicn-----vvaip 169
Qy 175 GTAQSDTTC--KNPLEPLPP 192
Db 170 gnsmdavctststsrmap 189

Search completed: October 4, 2002, 10:12:22
Job time: 85 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2002, 10:10:57 ; Search time 13.38 Seconds
(without alignments)
359.629 Million cell updates/sec

Title: US-09-299-139A-1

Perfect score: 1133

Sequence: 1 SOPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
'score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	197	2	US-08-505-606-1
2	771	68.0	415	4	US-08-006-353A-6
3	456	40.2	77	4	US-08-886-345-3
4	305	26.9	227	3	US-08-974-022-48
5	305	26.9	227	4	US-08-795-445A-48
6	305	26.9	227	4	US-08-795-447A-48
7	305	26.9	227	4	US-08-974-186-48
8	305	26.9	227	4	US-08-795-446B-48
9	305	26.9	235	4	US-09-326-394-4
10	305	26.9	461	1	US-08-385-229-2
11	305	26.9	461	2	US-08-650-000-2
12	305	26.9	461	4	US-09-042-785A-7
13	305	26.9	461	4	US-08-477-347-3
14	305	26.9	461	4	US-09-006-353A-4
15	305	26.9	461	4	US-08-476-862-2
16	305	26.9	461	6	5395760-2
17	305	26.9	486	1	US-08-243-010-1
18	305	26.9	518	1	US-08-385-229-4
19	295	26.0	474	2	US-08-650-000-4
20	295	26.0	474	4	US-09-042-785A-8
21	295	26.0	474	6	5395760-4
22	290.5	25.6	163	2	US-08-219-237B-5
23	290.5	25.6	163	4	US-08-477-347-13
24	290.5	25.6	163	4	US-08-476-862-4
25	290.5	25.6	163	4	US-08-468-560C-5
26	287	25.3	164	2	US-08-232-087A-9
27	286	25.2	211	4	US-09-286-529-20

28	285.5	25.2	300	2	US-08-794-796-2	Sequence 2, Appl
29	283	25.0	625	3	US-08-996-139-15	Sequence 15, Appl
30	283	25.0	625	4	US-08-995-659-15	Sequence 15, Appl
31	283	25.0	625	4	US-09-215-649A-15	Sequence 15, Appl
32	278	24.5	276	4	US-09-041-886-27	Sequence 27, Appl
33	278	24.5	277	4	US-09-042-785A-10	Sequence 10, Appl
34	278	24.5	277	4	US-09-006-353A-10	Sequence 10, Appl
35	277	24.4	299	4	US-09-286-529-17	Sequence 17, Appl
36	277	24.4	451	3	US-08-996-139-4	Sequence 4, Appl
37	277	24.4	451	4	US-08-995-659-4	Sequence 4, Appl
38	277	24.4	451	4	US-09-215-649A-4	Sequence 4, Appl
39	277	24.4	591	3	US-08-996-139-2	Sequence 2, Appl
40	277	24.4	591	4	US-08-995-659-2	Sequence 2, Appl
41	277	24.4	591	4	US-09-215-649A-2	Sequence 2, Appl
42	277	24.4	616	3	US-08-996-139-6	Sequence 6, Appl
43	277	24.4	616	4	US-08-995-659-6	Sequence 6, Appl
44	277	24.4	616	4	US-09-215-649A-6	Sequence 6, Appl
45	266	23.5	162	2	US-08-219-237B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-505-606-1
; Sequence 1, Application US/08505606
; Patent No. 5925351
; GENERAL INFORMATION:
; APPLICANT: BROWNING, Jeffrey L.
; APPLICANT: BENJAMIN, Christopher D.
; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
; TITLE OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS
; TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,606
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378,968
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B191
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-505-606-1

Query Match 100.0%; Score 1133; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.2e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQOAVPPYASENOTCRDQKEYEYEPQHRICCSRCPPGGTYVSAKCSIRDTVCATCAENS 60
DB 1 SQOAVPPYASENOTCRDQKEYEYEPQHRICCSRCPPGGTYVSAKCSIRDTVCATCAENS 60

QY 61 YNEHNYLTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
DB 61 YNEHNYLTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120

QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFONTSSPSARQCPHTRCENQGLVEAAPGTAQSD 180
DB 121 CPPGTEAELKDEVGKNNHCVPCKAGHFONTSSPSARQCPHTRCENQGLVEAAPGTAQSD 180

QY 181 TTCKNPLEPLPPMSGT 197
DB 181 TTCKNPLEPLPPMSGT 197

RESULT 2
US-09-006-353A-6
; Sequence 6, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-006-353A-6

Query Match 68.0%; Score 771; DB 4; Length 415;
Best Local Similarity 70.7%; Pred. No. 3.6e-65;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQOAVPPYASENOTCRDQKEYEYEPQHRICCSRCPPGGTYVSAKCSIRDTVCATCAENS 60
DB 28 SQQLVPPYRIENQTCWDQDKEYEYEPMDVCCSRCPGPEFVAVCSRSODTVCKTCPHNS 87

QY 61 YNEHNYLTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCTC--ELL 118
DB 88 YNEHNYLTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCTC--ELL 118
QY 119 SDCPGTEAELKDEVGKNNHCVPCKAGHFONTSSPSARQCPHTRCENQGLVEAAPGTAQ 178
DB 148 VUCQPGTEAELKDEVGKNNHCVPCKAGHFONTSSPSARQCPHTRCENQGLVEAAPGTAQ 178
QY 179 SDTCKNPLEP 189
DB 208 SDTCKNPLEP 218

RESULT 3
US-08-866-545-3
; Sequence 3, Application US/08866545
; Patent No. 6265535
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Takasaki, Wataru
; TITLE OF INVENTION: PEPTIDES AND PEPTIDE
; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,545
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009113-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265535e
US-08-866-545-3

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.7e-36;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNEHNYLTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAAWALE 111
DB 1 VCATCAENSYNEHNYLTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAAWALE 60

QY 112 CTHCELLSDCPPGTEAE 128
DB 112 CTHCELLSDCPPGTEAE 128

Db 61 CTHCELLSDCPPGTEAE 77

RESULT 4

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US-08-974-022-48
; Sequence 48, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, \
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022

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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/577,788
/
/ FILING DATE:
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winter, Robert B.
/ REFERENCE/DOCKET NUMBER: A-378
/
/ INFORMATION FOR SEQ ID NO: 48:
/
/ SEQUENCE CHARACTERISTICS:
/     LENGTH: 227 amino acids
/     TYPE: amino acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/
/ MOLECULE TYPE: protein
/
/ US-08-974-023-48

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Query Match	26.9%	Score 305;	DB 3;	Length 227;
Best Local Similarity	35.0%;	Pred. No. 1.6e-21;		
Matches	70;	Conservative	24;	Mismatches 78; Indels 28; Gaps 9;

QY	5	AVPEYASE-NOTCRDQKEYYEPOHRIKCSRCPPGTIVYSAKCSRIOTVCATCAENS	YNE 63
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QY	64	HNWYLTTCQLCR---PCDPVWGLEBIEIATTSKRKTCRCQPGMPCAAWALE-CTHCELLS	119
DB	86	LWNWVPECLSGGRSCSSDQV---ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR	141
QY	120	DCPPG-----TEAEIKDEVGKNNHCVPKAGHPQNTSSPSARCOPHTRENQGLVEAAP	174
DB	142	KCRPGFCVAPGTETSDVV-----CAKPCAPGTFSTNTSSDIDCRPHQICN-----VVAIP	191
QY	175	GTQSDTTC---KNPLEPLPP	192
DB	192	GNASRDACVCTSTGPTSRMAP	211

RESULT 5
US-08-795-445A-48
; Sequence 48, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.

APPLICANT: Lacey, David L.
 APPLICANT: Calzone, Frank J.
 APPLICANT: Chang, Ming-Shi
 TITLE OF INVENTION: OSTEOPROTEGERIN
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: 1840 Dehavilland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, V
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,445A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/577,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Robert B.
 REFERENCE/DOCKET NUMBER: A-378
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 227 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-795-445A-48

Query Match	26.9%;	Score 305;	DB 4;	Length 227;
Best Local Similarity	35.0%;	Pred. NO. 1.6e-21;		
Matches 70;	Conservative 24;	Mismatches 78;	Indels	

Qy	5	AVPPYASE-NQTQRDQBEKYYEQHRIICCSRCPPGYTVVSAKCSRIIRDVTVCATCAENSYN	63
Dd	28	AFTPYAPBPSTCR-LREYYDTAQMCCSKCSPGGHAKVFCITKTSDTVCDCSEDSTYTQ	85
Qy	64	HWNVLITCOLCR---PCDPWNGLEETAICTSKRKTQCRCOPGPFCAAWALE-CTHCELLS	119
Dd	86	LWNVPCLSCGRSSDQV----ETQACTFREQNRICTCRPGYCALSCKOEGRCRLCAPLR	141
Qy	120	DCPPG-----TEAEIKDEVCKGNNHCVPCKAQHFONTSPSARCQPHTRCENGLVEAAP	174
Dd	142	KCRGFGVARPGETSDVV-----CKPCAAGTFSTNTSTDLCRPHQTCN----VWAP	191
Qy	175	GTAQSDTTC--KNPLEPLPP	192
Dd	192	GNASRDVACTSTGPTSMAP	211

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RESULT      6
US-08-795-447A-48
; Sequence 48, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoproteger
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks

```

; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A-48

Query Match 26.9%; Score 305; DB 4; Length 227;
Best Local Similarity 35.0%; Pred. No. 1.6e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPVASE-NOTCRDOEKEYEYEPQHRIICSCRCPPGTYVSAAKCSRIKRTDVCATCAENSUNE 63
Db 28 AFTPYAPEPGSTCR--LREYDQTAQMCCSKCGSQHAKVFCTKTSVTVCDSCESTYVQ 85

QY 64 HNNYLTICQLCR---PCDPVMGLEIEIAPCTSKRRKTQCRCPQMFCAAWALE-CTHCELLS 119
Db 86 LWNWVPECLSCGSSGSSDQV-----ETQACTREQNRICTCRPGWCALSKQEGCRLCAPLR 141

QY 120 DCPPG-----TEAEKLDVGVGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAP 174
Db 142 KCRPGFGVAPGTETSDVV-----CKPCAPGTFSTNTSSDIDICRPHQICN-----VVAIP 191

QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVACTSTSPTRSMAP 211

RESULT 7
US-08-974-186-48
; Sequence 48, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-48

Query Match 26.9%; Score 305; DB 4; Length 227;
Best Local Similarity 35.0%; Pred. No. 1.6e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPVASE-NOTCRDOEKEYEYEPQHRIICSCRCPPGTYVSAAKCSRIKRTDVCATCAENSUNE 63
Db 28 AFTPYAPEPGSTCR--LREYDQTAQMCCSKCGSQHAKVFCTKTSVTVCDSCESTYVQ 85

QY 64 HNNYLTICQLCR---PCDPVMGLEIEIAPCTSKRRKTQCRCPQMFCAAWALE-CTHCELLS 119
Db 86 LWNWVPECLSCGSSGSSDQV-----ETQACTREQNRICTCRPGWCALSKQEGCRLCAPLR 141

QY 120 DCPPG-----TEAEKLDVGVGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAP 174
Db 142 KCRPGFGVAPGTETSDVV-----CKPCAPGTFSTNTSSDIDICRPHQICN-----VVAIP 191

QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVACTSTSPTRSMAP 211

RESULT 8
US-08-795-446B-48
; Sequence 48, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids

Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

Qy 5 AVPPYASE-NOTCRDOEKEYEYPOHRIICCSRCPPGTYYVSAKSRIRDTVCATCAENSYNE 63
 Db 28 AFTPYAPEPGTCTCR--LREYDQTAQMCCSKSPQGHAKVFCTKTSDTVCDSCEDSTYTQ 85
 Qy 64 HWNYLTICQLCR--PCDPVVMGLEIEIAPCTSKRKTQCRCPGMFCAAWALE-CTHCELLS 119
 Db 86 LWNWVPECLSGRCSSDQV-----ETQACTREQNRICTCRFGWYCALSKQEGCRLCAPLR 141
 Qy 120 DCPFG-----TEALKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAAP 174
 Db 142 KCRPGFGVARGTETSDV-----CKPCAPGTFTSNTSSDICTRPHOICN-----VWAP 191
 Qy 175 GTAQSDTTC--KNPLEPLPP 192
 Db 192 GNASMDAVCTSTSPTRSMAP 211

RESULT 13

US-08-477-347-3

Sequence 3, Application US/08477347

Patent No. 6232446

GENERAL INFORMATION:

APPLICANT: WALLACH, David

APPLICANT: BIGDA, Jacek

APPLICANT: BELETSKY, Igor

APPLICANT: METT, Igor

TITLE OF INVENTION: TNF LIGANDS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/477,347

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA: 08/115,685

APPLICATION NUMBER: 08/115,685

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 106271

FILING DATE: 08-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, G. Kevin

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: WALLACH-10

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-347-3

Query Match 26.9%; Score 305; DB 4; Length 461;

Best Local Similarity 35.0%; Pred. No. 3.4e-21;

Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

Qy 5 AVPPYASE-NOTCRDOEKEYEYPOHRIICCSRCPPGTYYVSAKSRIRDTVCATCAENSYNE 63
 Db 28 AFTPYAPEPGTCTCR--LREYDQTAQMCCSKSPQGHAKVFCTKTSDTVCDSCEDSTYTQ 85
 Qy 64 HWNYLTICQLCR--PCDPVVMGLEIEIAPCTSKRKTQCRCPGMFCAAWALE-CTHCELLS 119
 Db 86 LWNWVPECLSGRCSSDQV-----ETQACTREQNRICTCRFGWYCALSKQEGCRLCAPLR 141
 Qy 120 DCPFG-----TEALKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAAP 174
 Db 142 KCRPGFGVARGTETSDV-----CKPCAPGTFTSNTSSDICTRPHOICN-----VWAP 191
 Qy 175 GTAQSDTTC--KNPLEPLPP 192
 Db 192 GNASMDAVCTSTSPTRSMAP 211

RESULT 14

US-09-006-353A-4

Sequence 4, Application US/09006353A

Patent No. 6261801

GENERAL INFORMATION:

APPLICANT: WEI, YING-FEI

APPLICANT: YU, GUO-LIANG

APPLICANT: GENTZ, REINER

APPLICANT: RUBEN, STEVEN

TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/006,353A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF341

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-006-353A-4

Query Match 26.9%; Score 305; DB 4; Length 461;

Best Local Similarity 35.0%; Pred. No. 3.4e-21;

Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

Qy 5 AVPPYASE-NOTCRDOEKEYEYPOHRIICCSRCPPGTYYVSAKSRIRDTVCATCAENSYNE 63
 Db 28 AFTPYAPEPGTCTCR--LREYDQTAQMCCSKSPQGHAKVFCTKTSDTVCDSCEDSTYTQ 85
 Qy 64 HWNYLTICQLCR--PCDPVVMGLEIEIAPCTSKRKTQCRCPGMFCAAWALE-CTHCELLS 119
 Db 86 LWNWVPECLSGRCSSDQV-----ETQACTREQNRICTCRFGWYCALSKQEGCRLCAPLR 141

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OM protein - protein search, using sw model

Run on: October 4, 2002, 10:10:57 ; Search time 19.61 Seconds.
(without alignments)
965.303 Million cell updates/sec

Title: US-09-299-139A-1
Perfect score: 1133
Sequence: 1 SQQAVPPYASENQTCDQEQE.....QSDTTCKNPLEPLPPMSGT 197
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	435	2	I54182
2	305	26.9	461	1	A35356
3	295	26.0	474	2	B38634
4	290	25.6	459	2	I48854
5	278	24.5	277	2	A60771
6	243.5	21.5	305	2	A46476
7	226.5	20.0	651	2	JC7705
8	222.5	19.6	271	2	S12783
9	214.5	18.9	272	2	I48700
10	210.5	18.6	455	1	GQHT1
11	210	18.5	348	2	D28623
12	210	18.5	349	2	D36858
13	207	18.3	349	2	J27175
14	206	18.2	461	2	JC4302
15	201	17.7	277	2	I37552
16	201	17.7	454	1	GQMT1
17	196	17.3	595	2	A42086
18	195.5	17.3	255	2	I38426
19	189	16.7	325	2	B43692
20	187.5	16.5	314	2	I37383
21	184.5	16.3	461	1	GQRT1
22	183.5	16.2	326	1	GQVZML
23	181	16.0	335	2	A40036
24	179.5	15.8	256	2	B32393
25	171.5	15.1	425	1	A26431
26	166	14.7	493	2	JC5486
27	164	14.5	416	1	JN0006
28	162	14.3	327	2	A46484
29	148.5	13.1	427	1	GQHUN

30 145.5 12.8 324 2 JC2395
31 133 11.7 260 1 A46517
32 132.5 11.7 1111 2 T26972
33 129.5 11.4 1620 2 T27283
34 129 11.4 3084 1 MMMSA
35 128.5 11.3 1299 2 T43251
36 128 11.3 1274 2 T42017
37 126 11.1 3635 2 T10053
38 125.5 11.1 2180 2 T29764
39 124.5 11.0 899 2 G02428
40 124.5 11.0 915 2 JC6148
41 124.5 11.0 3707 2 S18252
42 124 10.9 1680 2 A43434
43 123.5 10.9 686 2 JC7569
44 123 10.9 722 2 I48324
45 122.5 10.8 915 1 A48225

ALIGNMENTS

RESULT 1

I54182

tumor necrosis factor receptor 2-related protein - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000

C;Accession: I54182

R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993

A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq

A;Reference number: I54182; MUID:93252381

A;Accession: I54182

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-435 <RES>

A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762

C;Genetics:

A;Gene: GDB:LTBR

A;Cross-references: GDB:L230195; OMIM:600979

A;Map position: 12p13.3-12p13.1

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 100.0%; Score 1133; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.4e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQEQEYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 60

Db 28 SQQAVPPYASENQTCDQEQEYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVVMGLEIAPCTSKRTQCRCQPMFCAAWALECTHCELLSD 120

Db 88 YNEHWNLTICQLCRPCDPVVMGLEIAPCTSKRTQCRCQPMFCAAWALECTHCELLSD 147

QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPTQASD 180

Db 148 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPTQASD 207

QY 181 TTCRNPLEPLPPMSGT 197

Db 208 TTCRNPLEPLPPMSGT 224

RESULT 2

A35356

tumor necrosis factor receptor 2 precursor [validated] - human

N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000

C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094

R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,

Science 248, 1019-1023, 1990

Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;

QY 15 TCRDOEKEYEYQHRIICSCRCPPGYVSAKCSIRDTVCATCAENSYNHWNLYTICQLC 74
 Db 25 TUCSD--KQYLHDGQ--CDLCPGSGRLTSHCTALEKTOCHPCDSGEFSAQWNRIRCHQH 80

QY 75 RPCDPMGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPPG-----TEAEL 129
 Db 81 RHCEPNOGLRVKKEGTAEADTCTCKEGOHCIT--SKDCEACQAHTPCIPGFGVMEMATET 138

QY 130 KDEVGKGNHCVPCAKAGHONTSSSARCPHTRCENOGVLVEAAGTCAQSDTTC 183
 Db 139 TDTV-----CHPCPVGFSSNOSSLFEKYPWTSCEDKNLEVLQGTSTQNVIC 186

RESULT 7
 JC7705
 death receptor-6 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 R:Accession: JC7705
 R:Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
 Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
 A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
 A:Reference number: JC7705; MUID:21308433; PMID:11414698
 A:Accession: JC7705
 A:Molecule type: mRNA
 A:Residues: 1-651 <BRI>
 A:CROSS-references: GB:AF349908
 C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily and is involved in cell death and/or survival signaling cascade.
 C:Genetics:
 A:Gene: dr-6
 C:Keywords: ovary
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:152-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
 F:332-350/Domain: transmembrane #status predicted <TM>
 F:410-475/Domain: death domain #status predicted <DED>
 F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 20.0%; Score 226.5; DB 2; Length 651;
 Best Local Similarity 28.8%; Pred. No. 6e-10;
 Matches 49; Conservative 26; Mismatches 62; Indels 33; Gaps 6;

QY 30 ICCSCRCPPGYVSAKCSIRDTVCATCAENSYNHWNLYTICQLCR-PCDPVPMGLEETAP 88
 Db 50 LICDKCPAGTYVSKHCTKSTLRECSPPDGTFTKHENGIERCHPCRKPCQ--LPMIEKTH 107

QY 89 CTSKRKTQCRQCPGMF-----CAAWALECTHCELLSDCP-----PGTEAELKDEVGKG 136
 Db 108 CVALTDRECTCLSGTFQINDTCVPYTV-----CPVGVGRKKGTETE----- 149

QY 137 NHCVPCKAGHONTSSSARCPHTRCENOGVLVEAAGTCAQSDTTCNP 186
 Db 150 DVRCRKLRLGTGSDVPSSVMKCKTYTDCFGKNNVVYKPGTKESDNVCXSP 199

RESULT 8
 SI2783
 OX40 antigen precursor - rat
 N:Alternate names: nerve growth factor receptor homolog
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: SI2783; S08036
 R:Mallett, S.; Fossum, S.; Barclay, A.N.
 EMBO J. 9, 1063-1068, 1990
 A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
 A:Reference number: SI2783; MUID:90214614
 A:Accession: SI2783
 A:Molecule type: mRNA
 A:Residues: 1-271 <MAL>
 A:CROSS-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:g57831

C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: growth factor receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-271/Product: OX40 antigen #status predicted <MAT>
 F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 19.6%; Score 222.5; DB 2; Length 271;
 Best Local Similarity 32.1%; Pred. No. 6.1e-10;
 Matches 53; Conservative 17; Mismatches 68; Indels 27; Gaps 5;

QY 21 KEYEYQHRIICSCRCPPGYVSAKCSIRDTVCATCAENSYNHWNLYTICQLCRPCDPV 80
 Db 28 KDTYPSGHK-CCRECQPGHGMVSRCDHTRDTVCHPCPEGYNEAVNYDT-CKQCTQCNRH 85

QY 81 MGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNHC 140
 Db 86 SGSELKQNCPTPTEDTVCCQR-----PGTQPR-QDSSSHKLGVD 122

QY 141 VPCKAGHONTSSSARCPHTRCENOGVLVEAAGTCAQSDTTCN 185
 Db 123 VPCPGHFSFGSNQA--CKPWTNCTLSGKQIRHPASNSLDTVCED 165

RESULT 9
 I48700
 gene ox40 protein - mouse
 N:Alternate names: OX40 antigen
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 R:Accession: I48700; I48334; S34377
 R:Calderhead, D.M.; Buhlmann, J.E.; van den Bortwegh, A.J.; Claassen, E.; Noelle, R.J.
 J. Immunol. 151, 5261-5271, 1993
 A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell
 A:Reference number: I48700; MUID:94044750
 A:Accession: I48700
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-272 <RES>
 A:CROSS-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
 R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
 Eur. J. Immunol. 25, 926-930, 1995
 A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
 A:Reference number: I48334; MUID:95255413
 A:Accession: I48334
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-14, 'G', 16-272 <RE2>
 A:CROSS-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
 C:Genetics:
 A:Gene: OX40
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 18.9%; Score 214.5; DB 2; Length 272;
 Best Local Similarity 31.7%; Pred. No. 2.5e-09;
 Matches 53; Conservative 16; Mismatches 67; Indels 31; Gaps 6;

QY 21 KEYEYQHRIICSCRCPPGYVSAKCSIRDTVCATCAENSYNHWNLYTICQLCRPCDPV 80
 Db 29 KHTYPSGHK-CCRECQPGHGMVSRCDHTRDTVCHPCPEGYNEAVNYDT-CKQCTQCNRH 86

QY 81 MGLEEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNHC 140
 Db 87 SGSELKQNCPTPTQDVTVCRCR-----PGTQPR-QDSSGYKLGVD 123

QY 141 VPCKAGHONTSSSARCPHTRCENOGVLVEAAGTCAQSDTTCN 185
 Db 124 VPCPGHFSFGSNQA--CKPWTNCTLSGKQIRHPASNSLDTVCED 166

RESULT 10

Q0HUT1

tumor necrosis factor receptor 1 precursor [validated] - human

N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1

N:Contents: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000

C:Accession: A38208

R:Fuchs, P.; Strehl, S.; Dworzak, M.; Hummler, A.; Ambros, P.F.

Genomics 13, 219-224, 1992

A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to chromosome 10

A:Reference number: A38208; MUID:92250049

A:Accession: A38208

A:Molecule type: DNA

A:Residues: 1-455 <FOC>

A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g339748

R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, C.

Cell 61, 351-359, 1990

A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor

A:Reference number: A34899; MUID:90235284

A:Accession: A34899

A:Molecule type: mRNA

A:Residues: 1-455 <LOE>

A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754

A:Experimental source: Placenta

A:Note: part of this sequence, including the amino end of the mature protein, confirmed

R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.

Cell 61, 361-370, 1990

A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.

A:Reference number: A34900; MUID:90235285

A:Accession: A34900

A:Molecule type: mRNA

A:Residues: 1-455 <SCH>

A:Cross-references: GB:M3294; NID:g339744; PIDN:AAA03210.1; PID:g339745

R:Hummler, A.; Maurer-Pogoy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.

DNA Cell Biol. 9, 705-715, 1990

A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptors

A:Reference number: A36555; MUID:91090841

A:Accession: A36555

A:Molecule type: mRNA

A:Residues: 1-455 <HIM>

A:Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756

A:Accession: C36555

A:Molecule type: protein

A:Residues: 30-38; 41-53; 'X', 55-79; 'XX', 82-94; 'NK', 'XX', 100-104; 107-128; 162-167; 'X', 169-200

A:Note: the purified protein, called tumor necrosis factor binding protein, is a soluble

R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.

Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990

A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant protein

A:Reference number: A38281; MUID:91017509

A:Accession: A38281

A:Molecule type: mRNA

A:Residues: 1-455 <GRA>

A:Cross-references: GB:M37764

A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372

R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann

EMBO J. 9, 3269-3278, 1990

A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I

A:Reference number: S12057; MUID:91006021

A:Accession: S12057

A:Molecule type: mRNA

A:Residues: 1-455 <NOP>

A:Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224

A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w

R:Kemper, O.; Wallach, D.

Gene 134, 209-216, 1993

A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne

A:Reference number: JT0758; MUID:94085779

A:Accession: JT0758

A:Molecule type: DNA

A:Residues: 1-13 <KEM>

R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.

Eur. J. Immunol. 20, 1167-1174, 1990

A>Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequ
A:Reference number: A60231; MUID:90292116
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43,'X','45-53','X','55-57 <SEC>
R:Gatanga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.;
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A>Title: Purification and characterization of an inhibitor (soluble tumor necrosis fa
tients.
A:Reference number: A38258; MUID:91062364
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyrell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A>Title: Isolation and characterization of a tumor necrosis factor binding protein fr
A:Reference number: A60594; MUID:89171156
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43,'X','45-53','V','55-57','KK','60 <OLS>
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A>Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A:Reference number: A35010; MUID:90110215
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A>Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purifie
A:Reference number: JC2404; MUID:95128033
A:Accession: JC2404
A:Molecule type: protein
A:Residues: 41-53,'X','55-144','X','146-150','X','152-186','X','188-201 <KAJ>
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-45/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #stat
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
E:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

	Query Match	18.6%	Score 210.5;	DB 1;	Length 455;
	Best Local Similarity	32.6%;	Pred. No. 7.3e-09;		
	Matches 61;	Conservative 19;	Mismatches 84;	Indels 23;	Gaps 9;
Qy	18 DOEK-----EYEPQHR-ICCSRCPGTGYYSAC-SRIRDTVCATCAENSNEHWNY	67	:	:	:
Dd	36 DEKRDSVCPQGKIHPQNNSICTCHKGTYLYNDGPGQDTCRECSGSFTASENH	95	:	:	:
Qy	68 LTICOLRCPCDPVMGLEETAPCTSKRTCKRCQGMFCANAWA---LECTHCELLSDCPPG	124	:	:	:
Dd	96 LRHLUSCSKCRKEMGOVELISSTVDRTVCGCRKNQI RHYWSENLFOCFNCSL---CLNG	152	:	:	:
Qy	125 TEALKDEVGKGNHCVPCKAGHF--QNTSSPSARCOPIHTRCNQGL--VEAAPGTAQSD	180	:	:	:

C;Accession: JC4302; PC4093

R;Suter, B.; Pauli, U.

Gene 163, 263-266, 1995

A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A;Reference number: JC4302; MUID:96011645

A;Accession: JC4302

A;Molecule type: mRNA

A;Residues: 1-461 <SUT>

A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753

A;Accession: PC4093

A;Molecule type: protein

A;Residues: 1-7 <SU2>

A;Experimental source: kidney cell line 15

C;Genetics:

A;Gene: tnfr

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>

F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>

F;44-82/Domain: NGF receptor repeat homology <NG1>

F;84-126/Domain: NGF receptor repeat homology <NGF>

F;211-231/Domain: transmembrane #status predicted <TM>

F;361-447/Domain: signal transduction #status predicted <SIT>

F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.2%; Score 206; DB 2; Length 461;

Best Local Similarity 29.4%; Pred. No. 1.6e-08;

Matches 57; Conservative 22; Mismatches 77; Indels 38; Gaps 9;

QY 18 DQEK-----EYEPQHR-ICSRCPPGTYVSACK-SRIRDVVCATCAENSYNEHWN 67

DB 36 DREKRSLCPQGYKSHPNRSICCTCKHGYLHNDCLGDLTDRECDNGTFTASENH 95

QY 68 LTICQLCRPCDPVNGLEIAPCISKRTQRCQPMFCAAWA---LECTHCELLSDCPPG 124

DB 96 LTQCLSKCKRSEMSQVEISPTVDRTVCGCRKNQYKYNWSETFQCLNCSL---CPNG 152

QY 125 TE----AELKDEVGKGNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQ-- 178

DB 153 TVQLPCLQEKQDTI-----CNCHSGFFLR-----DKECVSCVNCNADKRLCPATSETR 201

QY 179 -----SDTTCKNPL 187

DB 202 NDFQDTGTGTVLLPL 215

RESULT 15

I37552

OX40 homolog - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000

C;Accession: I37552

R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat

Eur. J. Immunol. 24, 677-683, 1994

A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment c

A;Reference number: I37552; MUID:941170844

A;Accession: I37552

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-277 <RES>

A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958

C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 17.7%; Score 201; DB 2; Length 277;

Best Local Similarity 28.3%; Pred. No. 2.6e-08;

Matches 49; Conservative 21; Mismatches 73; Indels 30; Gaps 5;

QY 26 PQHRICSRCPPGTYVSACKSRIRDVVCATCAENSYNEHWNLTICOLCRPCDPVNGLEE 85

DB 37 PSNDRCHECRPGNGVMYSRGSRQNTVCRPCGPGFYNDVYSSKP-CKPCTWCNLRSGSER 95

QY 86 IAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNHCVPCKA 145

DB 96 KQLCTATQDTVCRCRAG-----TQPLDSYKRGVD-----CAPCPP 130

QY 146 GHFONTSSPSARCPHTRCENQGLVEAAPGTAQSDTTC--KNPLEPLPEMSG 196

DB 131 GHF--SPGDNOACKPWTNCTLAGKHHTLQPASNSSDAICEDRDPATOPQETQG 181

Search completed: October 4, 2002, 10:11:46

Job time: 49 sec

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: October 4, 2002, 10:11:22 ; Search time 11.94 Seconds
(without alignments)
638.840 Million cell updates/sec

Title: US-09-299-139A-1

Perfect score: 1133

Sequence: 1 SQQAVPPYASENQCRDQE.....QSDTCKNPLEPLPPMSMST 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	1133	100.0	435	1	TNR3_HUMAN
2	771	68.0	415	1	TNR3_MOUSE
3	305	26.9	461	1	TR1B_HUMAN
4	295	26.0	474	1	TR1B_MOUSE
5	283	25.0	625	1	TR1L_MOUSE
6	278	24.5	277	1	TNR5_HUMAN
7	277	24.4	616	1	TR1L_HUMAN
8	251.5	22.2	269	1	TNR5_BOVIN
9	243.5	21.5	289	1	TNR5_MOUSE
10	230.5	20.3	283	1	TR1A_HUMAN
11	222.5	19.6	271	1	TNR4_RAT
12	214.5	18.9	272	1	TNR4_MOUSE
13	210.5	18.6	455	1	TR1A_HUMAN
14	210	18.5	349	1	VC22_VARV
15	206	18.2	461	1	TR1A_PIG
16	203	17.9	323	1	TNR6_BOVIN
17	201	17.7	277	1	TNR4_HUMAN
18	201	17.7	454	1	TR1A_MOUSE
19	196	17.3	595	1	TNR8_HUMAN
20	195.5	17.3	255	1	TNR9_HUMAN
21	194	17.1	332	1	TNR9_PIG
22	189	16.7	325	1	VT2_SFVK
23	188	16.6	471	1	TR1A_BOVIN
24	184.5	16.3	461	1	TR1A_RAT
25	183.5	16.2	326	1	VT2_MYXVL
26	181	16.0	335	1	TNR6_HUMAN
27	179.5	15.8	256	1	TNR9_MOUSE
28	171.5	15.1	425	1	TR16_RAT
29	167.5	14.8	440	1	T10B_HUMAN
30	164	14.5	416	1	TR16_CHICK
31	162	14.3	327	1	TNR6_MOUSE
32	148.5	13.1	427	1	TR16_HUMAN
33	145.5	12.8	324	1	TNR6_RAT

34 143.5 12.7 468 1 T10A_HUMAN
35 140.5 12.4 417 1 TR12_HUMAN
36 130 11.5 3695 1 LMA5_HUMAN
37 129 11.4 3084 1 LMA1_MOUSE
38 128 11.3 260 1 TNR7_HUMAN
39 126 11.1 1799 1 LMB2_MOUSE
40 126 11.1 3718 1 LMA5_MOUSE
41 125 11.0 714 1 DLL1_RAT
42 124.5 11.0 913 1 PCK5_HUMAN
43 124.5 11.0 1696 1 PCK5_BRACL
44 124.5 11.0 3707 1 PGBM_MOUSE
45 124 10.9 1680 1 PUR2_DROME

ALIGNMENTS

RESULT 1

TNR3_HUMAN
ID TNR3_HUMAN STANDARD: PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lymphotoxin-beta receptor precursor (Tumor necrosis factor receptor)
DE 2 related protein) (Tumor necrosis factor C receptor).
GN LTBR OR TNFR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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EMBL; L04270; AAA36757.1; -;
HSSP; P25942; LCDF.
MIM; 600979; -;
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00650; TNFR_NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL 1 30 POTENTIAL.
CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
TRANSMEM 228 248 POTENTIAL.

```
FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL)..
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 100.0%; Score 1133; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 9.4e-90;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENQTCRDOEKYEYEPQHRIICSCRCPPGTYVSAAKSRIRDTVCATCAENS 60
Db 28 SQPQAVPPYASENQTCRDOEKYEYEPQHRIICSCRCPPGTYVSAAKSRIRDTVCATCAENS 87
QY 61 YNEHNYLTICQLCRPCDPVGMGLEIAICTSKRKTQCRQCPGMCAAWALECTHCELLSD 120
Db 88 YNEHNYLTICQLCRPCDPVGMGLEIAICTSKRKTQCRQCPGMCAAWALECTHCELLSD 147
QY 121 CPPGTEAEALKEDEKGVGNHCVPCRGAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPPGTEAEALKEDEKGVGNHCVPCRGAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 2
ID TNR3_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lymphotoxin-beta receptor precursor.
GN LTR OR TNFR OR TNFRSF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
```

```
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U29173; AAA68964.1; -.
CC EMBL; L38423; AAB00846.1; -.
CC EMBL; U30798; AAA81334.1; -.
CC HSSP; P25942; 1CDF.
CC MGD; MGI:104875; Ltbr.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 3.
CC ProDom; PD000771; TNFR_C6; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 3.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL
FT CHAIN 1 30 POTENTIAL.
FT DOMAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.
FT TRANSMEM 224 244 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 170 TNFR-CYS 3.
FT REPEAT 171 213 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 68.0%; Score 771; DB 1; Length 415;
Best Local Similarity 70.7%; Pred. No. 6.7e-59;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQPQAVPPYASENQTCRDOEKYEYEPQHRIICSCRCPPGTYVSAAKSRIRDTVCATCAENS 60
Db 28 SQPQAVPPYASENQTCRDOEKYEYEPQHRIICSCRCPPGTYVSAAKSRIRDTVCATCAENS 87
QY 61 YNEHNYLTICQLCRPCDPVGMGLEIAICTSKRKTQCRQCPGMCAAWALECTHCELLSD 118
Db 88 YNEHNYLTICQLCRPCDPVGMGLEIAICTSKRKTQCRQCPGMCAAWALECTHCELLSD 147
QY 119 SDCPPGTEAEALKEDEKGVGNHCVPCRGAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQ 178
Db 148 VLCQPGTEAEVTDIMDTDNCVCPKFGFQNTSSPRARCOPHTRCETQGLVEAAPGTSY 207
QY 179 SDCPPGTEAEVTDIMDTDNCVCPKFGFQNTSSPRARCOPHTRCETQGLVEAAPGTSY 207
Db 208 SDCPPGTEAEVTDIMDTDNCVCPKFGFQNTSSPRARCOPHTRCETQGLVEAAPGTSY 207

RESULT 3
ID TR1B_HUMAN STANDARD; PRT; 461 AA.
ID TR1B_HUMAN STANDARD; PRT; 461 AA.
AC P20333;
DT 01-FEB-1991 (Rel. 17, Created)
```

01-AUG-1991 (Rel. 19, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor binding protein 2) (TNFR2) (p75) (CD120B) (Etanercept).
 TNFRSF1B OR TNFR2 OR TNFR.
 GN TNFRSF1B OR TNFR2 OR TNFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RA "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RT Science 248:1019-1023(1990).
 RL
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kolno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RA "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RL [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=96299745; PubMed=8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
 RA Brodeur G.M.;
 RA "Physical mapping and genomic structure of the human TNFR2 gene.";
 RT Genomics 35:94-100(1996).
 RL [4]
 RN SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=90349572; PubMed=2166946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RA "Complementary DNA cloning of a receptor for tumor necrosis factor
 RT and demonstration of a shed form of the receptor.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 RL [5]
 RN SEQUENCE OF 27-31.
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RA "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface
 RT tumor necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [6]
 RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RA "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [7]
 RN CHARACTERIZATION.
 RX MEDLINE=93016040; PubMed=1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RA "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
 RN TRAF2.
 RX MEDLINE=99221490; PubMed=10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RA "Structural basis for self-association and receptor recognition of
 RT human TRAF2.";

Nature 398:533-538(1999).
 -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
 APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 -!- SUBCELLULAR LOCATION: Type I membrane protein.
 -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 LEVEL ON THREONINE RESIDUES.
 -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
 Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
 arthritis (RA). Enbrel consist of the extracellular ligand-binding
 portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to
 TNF-alpha and blocks its interactions with receptors.
 -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
 -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
 WWW="http://www.enbrelinfo.com/".

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 or send an email to license@isb-sib.ch).

 DR EMBL; M32315; AAA59929.1; -
 DR EMBL; M35857; AAC63262.1; -
 DR EMBL; U52165; AAC50622.1; -
 DR EMBL; U52156; AAC50622.1; JOINED.
 DR EMBL; U52157; AAC50622.1; JOINED.
 DR EMBL; U52158; AAC50622.1; JOINED.
 DR EMBL; U52159; AAC50622.1; JOINED.
 DR EMBL; U52160; AAC50622.1; JOINED.
 DR EMBL; U52161; AAC50622.1; JOINED.
 DR EMBL; U52162; AAC50622.1; JOINED.
 DR EMBL; U52163; AAC50622.1; JOINED.
 DR EMBL; U52164; AAC50622.1; JOINED.
 DR EMBL; M55994; AAA36755.1; -
 DR PIR; A35356; A35356.
 DR PIR; A36007; A36007.
 DR PIR; A36475; A36475.
 DR PIR; B35010; B35010.
 DR PIR; A23666; A23666.
 DR PDB; 1CA9; 12-APR-99.
 DR MM; 191191; -
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 4.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Phosphorylation; Pharmaceutical; 3D-structure.
 FT SIGNAL 1
 FT CHAIN 22
 FT DOMAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT TRANSMEM 258 287 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 288 461 POTENTIAL.
 FT REPEAT 39 76 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 77 118 TNFR-CYS 1.
 FT REPEAT 119 162 TNFR-CYS 2.
 FT REPEAT 163 201 TNFR-CYS 3.
 FT DISULFID 40 53 TNFR-CYS 4.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 110 BY SIMILARITY.
 FT DISULFID 100 118 BY SIMILARITY.
 FT DISULFID 120 126 BY SIMILARITY.
 FT DISULFID 134 143 BY SIMILARITY.
 FT DISULFID 137 161 BY SIMILARITY.
 FT DISULFID 164 179 BY SIMILARITY.
 FT CARBOHYD 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 171

DE Tumor necrosis factor receptor superfamily member 11A precursor
DE (receptor activator of NF- κ B) (osteoclast differentiation factor
DE receptor) (ODFR).
GN TNFRSF11A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tonetsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=9907247; PubMed=9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
CC -!- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS
CC OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-
CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
CC INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
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CC EMBL; AF019046; AAB86810.1; -.
CC HSSP; P25942; 1CDF.
CC MGD; MGI:1314891; Tnfrsf11a.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 3.
CC ProDom; PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 625
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPRACELLULAR MEMBER 11A.
FT POTENTIAL.
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS 1.
FT REPEAT 72 113
FT TNFR-CYS 2.
FT REPEAT 115 152
FT TNFR-CYS 3.
FT REPEAT 155 195
FT TNFR-CYS 4.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 175 175

SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;
Query Match 25.0%; Score 283; DB 1; Length 625;
Best Local Similarity 32.68; Pred. No. 4e-17; Mismatches 85; Indels 14; Gaps 4;
Matches 60; Conservative 25;
Qy 4 QAVPPYASENCTCRDOEREYVEPQHRICCSRPPGTYVSASAKSRIRDTVCATCAENSYNE 63
Db 30 QVTPECTQE-----RHYEHLGR-CSSRCEPKYLSKKTPTSDSVCLPCGDPDEYLD 79
Qy 64 HWNYITICQLCRPCDPVVMGLBEIAPCTSKRTQCRQCPGMFCAAWALBETHCELLSDCCP 123
Db 80 TWNEEDKCLLHKVCDAGKALVAVDPGNHTAPRCACCTAGYH---WNSDECCRRNTECAP 136
Qy 124 GTEAELKDEVKGNHNCVPCCKAGHFQNTSSPSARCOPTRCENQGLVEAAPTASDTTC 183
Db 137 GFQAQHLQQLNR-DTVCTPCLLGFSDVFSSTDKCKPWTNCTLLGLKLEAHQGTTESDVVC 195
Qy 184 KNPL 187
Db 196 SSSM 199
RESULT 6
ID TNRS_HUMAN STANDARD; PRY; 277 AA.
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).
DE TNFRSF5 OR CD40.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Hovden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasalho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.E.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLean K., McMurray A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";

CC	-!	SIMILARITY:	CONTAINS 4 TNFR-CYS REPEATS.
CC	----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	or send an email to license@isb-sib.ch).	
CC	-----		
DR	EMBL;	AFO18253; AAB6809.1; -.	
DR	HSSP;	P25942; ICDF.	
DR	MIM;	603499; -.	
DR	MIM;	174810; -.	
DR	MIM;	602080; -.	
DR	InterPro;	IPR001368; TNFR_C6.	
DR	Pfam;	PF00020; TNFR_C6; 4.	
DR	ProDom;	PD000771; TNFR_C6; 1.	
DR	SMART;	SM00208; TNFR; 4.	
DR	PROSITE;	PS00652; TNFR_NGFR_1; 1.	
DR	PROSITE;	PS00030; TNFR_NGFR_2; 1.	
KW	Receptor;	Glycoprotein; transmembrane; Repeat; Signal; Polymorphism;	
KW	Disease mutation.		
FT	SIGNAL	1 29	POTENTIAL.
FT	CHAIN	30 616	TUMOR NECROSIS FACTOR RECEPTOR
FT			SUPERFAMILY MEMBER 11A.
FT	DOMAIN	30 212	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	213 233	POTENTIAL.
FT	DOMAIN	234 616	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	34 68	TNFR-CYS 1.
FT	REPEAT	71 112	TNFR-CYS 2.
FT	REPEAT	114 151	TNFR-CYS 3.
FT	REPEAT	154 194	TNFR-CYS 4.
FT	DISULFID	34 46	BY SIMILARITY.
FT	DISULFID	47 60	BY SIMILARITY.
FT	DISULFID	50 68	BY SIMILARITY.
FT	DISULFID	71 86	BY SIMILARITY.
FT	DISULFID	92 112	BY SIMILARITY.
FT	DISULFID	114 127	BY SIMILARITY.
FT	DISULFID	133 151	BY SIMILARITY.
FT	CARBOHYD	105 105	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	174 174	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	13 21	ALLCALL --> ALLLCALLALLCALL (IN PDB2).
FT			/FTID-VAR_011516.
FT	VARIANT	16 21	LLCALL --> LLLCALLL (IN FEO).
FT			/FTID-VAR_011517.
FT	VARIANT	192 192	A -> V
FT			/FTID-VAR_011518.
FT	SEQUENCE	616 AA; 66033 MW; E3DE9A/A08196F81 CRC64;	
SO			
Query Match 24.4%; Score 277; DB 1; Length 616;			
Best Local Similarity 31.7%; Pred. No. 1.3e-16;			
Matches 60; Conservative 28; Mismatches 87; Indels 14; Gaps 4;			
QY	4	QAVPPYASNQTRCDKQEYYEPOHRIICCRCPPGTIVYSAKCSIRDVTCATCAENSYN 63	
Db	29	QIAPPCTSE-----KHYEHLGR--CKNKCEPGKYMSKKTTSDSVCLPCGPDPDYLD 78	
QY	64	HWNYLTITCOLCRCPDPMVGLEETAPCTSKRTQCRCQPGMFCAAWALECHTCELLSDCPP 123	
Db	79	SNWEEDCKLHKVCDTGKALVVAGNSTTPRRCACTAGYH---WSODCECCRNTBCAP 135	
QY	124	GTEAEELDKGVGNHNCVPCKAGHFQNTSSPARCQPHTRCENGLVEAAPGTAQSDDTC 183	
Db	136	GLGAQHFLQLNK-DTVCKPCLAGVFSDAFSSDTCKRPWTNCTFLGKRVEHHGTESDAVC 194	
QY	184	KNPLEPLPP 192	
Db	195	SSSLPARKP 203	

RESULT	8
ID	TNR5_BOVIN
STANDARD:	PRT; 269 AA.
Q28203;	
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Tumor necrosis factor receptor superfamily member 5 precursor
DE	(CD40L receptor) (B-cell surface antigen CD40) (Fragment).
GN	TNFRSF5 OR CD40.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=97281252; PubMed=9135560;
RX	Hirano A., Brown W.C., Estes D.M.;
RA	"Cloning, expression and biological function of the bovine CD40
RT	homologue: role in B-lymphocyte growth and differentiation in
RT	cattle.";
RL	Immunology 90:294-300(1997).
CC	-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; U57745; AAC48710.1; --
DR	HSP; P25942; ICDF.
DR	InterPro; IPR001368; TNFR_c6.
DR	Fam; PF00020; TNFR_c6; 4.
DR	ProDom; PD000771; TNFR_c6; 1.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.
DR	PROSITE; PS00050; TNFR_NGFR_2; 1.
KW	Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT	SIGNAL 1
FT	CHAIN 20 >269
FT	POTENTIAL.
FT	TUMOR NECROSIS FACTOR RECEPTOR
FT	SUPERFAMILY MEMBER 5.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).
FT	TNFR-CYS 1.
FT	TNFR-CYS 2.
FT	TNFR-CYS 3.
FT	TNFR-CYS 4.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	N-LINKED (GLCNAC...) (POTENTIAL).
FT	N-LINKED (GLCNAC...) (POTENTIAL).
FT	NON_TER 269
FS	SEQUENCE 269 AA; 22983 MW; 746903F30F95F387 CRC64;
Query Match	22.2%; Score 251.5; DB 1; Length 269;
Best Local Similarity	33.1%; Pred. No. 9.2e-15;
Matches 55; Conservative 21; Mismatches 81; Indels 9; Gaps 4;	

QY 20 EKEYEYEPQHRICCSRCPPGTYVSAKCSRI RD TVCATCAENSYN EHWNYLTICQLCRPCDP 79

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Db 28 EKQY--PWNLCDDCPGQKLVNDTEVSKTECSGKGFEIETWNRKCYCHEHYCNP 85
      ||:| | : : || |||| : | : : | | : : | | | | | | | | | | | | | | | |
QY 80 VNGLEIEIAPCTSKRTQCRQCPGMFCAAWALBCTHCELLSDCPPGTARELKDVGK--N 137
      :| | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 NGLRIQSEGLTNTDTCVCEGQCTSHT--CESCTHSLCLPFGVK--QIATGLLD 140
      :| | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 138 NHCVPCKAGHFONTSSPARGCPHTRCENQGLVEAAPGTAQSDTTC 183
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 141 TVCEPCPLGFFSNSSAFEKCHRWTSCKERKGLVEQHVGINKTDVVC 186
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
ID TNRS_MOUSE STANDARD; PRT; 289 AA.
AC P27512;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation.";
RJ J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN-BALB/C;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RJ J. Immunol. 149:3921-3926(1992).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M83312; AAB08705.1; -
DR EMBL; M94126; AAA37404.1; -
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
DR PIR; A46476; A46476.
DR HSP; P25942; 1CDF.
DR MGD; MGI:88336; Tnfrsf5.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.

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FT SIGNAL 1 19
FT CHAIN 20 289
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 5.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS 1.
FT REPEAT 25 60
FT TNFR-CYS 2.
FT REPEAT 104 144
FT TNFR-CYS 3.
FT REPEAT 145 187
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153
SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

Query Match 21.5%; Score 243.5; DB 1; Length 289;
Best Local Similarity 31.0%; Pred. No. 4.7e-14;
Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;

QY 15 TCRDQEKVEYEPQHRICCSRCPPGYVSAAKSRIRDTVCATCAENSYNHWNLYTICQLC 74
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 25 TCSD--KOYLHDGQ--CCDLQCPGSLTSHCTALEKTCHQPCDSEFSQAWNREIRCHQH 80
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 75 RCPDPMGLEEIAPTSKRKTKQCRQCPGMFCAAWALECTHCELLSDCPPG-----TEAL 129
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 81 RHCEPNQGLRVKKEGTAEISDVTCTCKEGQHCT--SKDCEACAQHTPCIPFGVMEATET 138
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 130 KDEVCKGNHVCVPCKAGHFONTSSPARGCPHTRCENQGLVEAAPGTAQSDTTC 183
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 139 TDTV-----CHPCVPVGFSSNOISLFKCYPTWTSCKDNKLVQLQKTSQTNVIC 186
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
TR14_HUMAN
ID TR14_HUMAN STANDARD; PRT; 283 AA.
AC Q92956; Q90M65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor
DE (Herpesvirus entry mediator) (Tumor necrosis factor receptor-like 2)
DE (TR2).
GN TNFRSF14 OR HVEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=97053782; PubMed=8998196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT the TNF/NGF receptor family.";
RJ Cell 87:427-436(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97306336; PubMed=9162061;
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA Porter T.G., Truneh A., Young P.R.;
RT "A newly identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation.";
RJ J. Biol. Chem. 272:14272-14276(1997).
RN [3]

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RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR TNFSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.
CC THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO
CC CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN T CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC IN LUNG, SPLEEN, AND THYMUS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; U70321; AAB58354.1; -.
CC EMBL; U81232; AAD00505.1; -.
CC EMBL; AF153978; AAF75588.1; -.
CC HSSP; P25942; 1CDF.
CC
CC MIM: 602746.
CC
CC InterPro: IPR001368; TNFR_C6.
CC Pfam: PF00020; TNFR_C6; 3.
CC ProDom: PD000771; TNFR_C6; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
CC SIGNAL
CC CHAIN 1 38
CC TISSUE NECROSIS FACTOR RECEPTOR
CC SUPERFAMILY MEMBER 14.
CC EXTRACELLULAR (POTENTIAL).
CC CYTOPLASMIC (POTENTIAL).
CC TNFR-CYS 1.
CC TNFR-CYS 2.
CC TNFR-CYS 3.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC K -> R (IN REF. 1).
CC CONFLICT 17 17
CC SEQUENCE 283 AA; 30392 MW; 46CEI3C2C70242C1 CRC64;

Query Match 20.3%; Score 230.5; DB 1; Length 283;
Best Local Similarity 30.1%; Pred. No. 5.9e-13;
Matches 56; Conservative 17; Mismatches 66; Indels 51; Gaps 6;

QY 7 PPYASENQTCDQREKEYEYPOHRIICCRPGTGVYSAKSRIRDTVCATCAENSYNEHWN 66
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 33 PCYAPALPSCK--EDEV--PVGSECCPKSPGYRKEACGELTGTCVCPGPGTYIAHLN 88
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 -----IVQDGDHCAACRA---YATSPGQVRVQ-----KGTESQDTLCON- 164
QY 187 LEPLPP 192
II

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Db 165 ---CPP 167

RESULT 11
TNRA_RAT
ID TNRA_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE receptor) (OX40 antigen) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-T-cell;
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RT lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMOB J. 9:1063-1068(1990).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; X17037; CAA34897.1; -.
CC PIR: S08036; S08036.
CC PIR: S12783; S12783.
CC HSSP; P19438; 1EXT.
CC InterPro: IPR001368; TNFR_C6.
CC Pfam: PF00020; TNFR_C6; 3.
CC ProDom: PD000771; TNFR_C6; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 3.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
CC SIGNAL
CC CHAIN 1 19
CC TISSUE NECROSIS FACTOR RECEPTOR
CC SUPERFAMILY MEMBER 4.
CC EXTRACELLULAR (POTENTIAL).
CC CYTOPLASMIC (POTENTIAL).
CC TNFR-CYS 1.
CC TNFR-CYS 2.
CC TNFR-CYS 3 (INCOMPLETE).
CC TNFR-CYS 4.
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 143 143
CC SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 19.6%; Score 222.5; DB 1; Length 271;
Best Local Similarity 32.1%; Pred. No. 2.7e-12;
Matches 53; Conservative 17; Mismatches 68; Indels 27; Gaps 5;

QY 21 KEYEYPOHRIICCRPGTGVYSAKSRIRDTVCATCAENSYNEHWNLTICOLCRPCDPV 80
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 28 KDTYPSGHK--CCRCQPGHGMVSRCDTRDTVCHPCEPGFYNEAVNYDT--CKQCTQCNRH 85
QY 81 MGLEIAPCTSKRKTQCRQCQPGMFCAAWALECTHCELLSDCPCGTAEKLDKDEVGKGNHC 140
II

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Db 153 TVHLSQCE--KONTVCT-CHAGFFLRENECVSCNCKSLSECTKLCPLQIENVKGTDSG 209
Oy 181 TTCKNPL 187
Db 210 TTVLPL 216

RESULT 14
VC22_VARV STANDARD; PRT; 349 AA.
AC P34015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE protein C22/B28 homolog.
GN G4R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93202281; PubMed=8384129;
RA "Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; X69198; CAA49137.1; .
CC EMBL; X67117; CAA47540.1; .
CC PIR; D36858; D36858.
CC PIR; S35987; S35987.
CC PIR; S46888; S46888.
CC HSSP; P25942; ICDF.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 2.
CC ProDom; PD000771; TNFR_C6; 1.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
KW REPEAT.
KW REPEAT.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
SQ SEQUENCE 349 AA; 38189 MW; D45D40B5C6E780EF CRC64;

Query Match 18.5%; Score 210; DB 1; Length 349;
Best Local Similarity 29.08; Pred. No. 4e-11;
Matches 45; Conservative 20; Mismatches 80; Indels 10; Gaps 5;

Oy 8 PYASENQCROEKEYEYPOHRIICSCRPCTGYVSAAKSRIRDTVCAPCAENSYNEHWNY 67
Db 24 PYTPNGKCKDTYK-----RHNLCLSCPPGTYASRLCDKSTNTQCTPCGSGTFTSRNH 79
Oy 68 LTICOLCR-PCDPVNGLEIEAPCTSKRTQCRCQPGMFC-AWALECHTCELLSDCPPT 125
Db 80 LPACLSCNRCN--SNQVETRSCNTHNRICECSFGYICLLKSGGCKACVSOQKAC--GI 135
Oy 126 EAEKDEKGVGNHCVCPCKAGHFONTSPSPARCP 160
Db 136 GYGVSGTSGDVICSPCGFGTYSHTVSSADKCEP 170
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RESULT 15
TRIA_PIG STANDARD; PRT; 461 AA.
AC P50555;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-RI)
DE (p55).
GN TNFRSF1A OR TNFR1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96011645; PubMed=7590278;
RA Suter B., Pauli U.H.;
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT receptor.";
RL Gene 163:263-266(1995).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMODIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC
CC EMBL; U19994; AAC48499.1; .
CC HSSP; P19438; 1TNR.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00531; death; 1.
CC Pfam; PF00020; TNFR_C6; 3.
CC ProDom; PD000771; TNFR_C6; 1.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 3.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR 1.
FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 233 POTENTIAL.
FT DOMAIN 234 461 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 195 TNFR-CYS 4.
FT DOMAIN 340 350 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 362 447 DEATH.
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Result No.	Query %			Length	DB	ID	Description
	Score	Match					
1	291.5	25.7	425	4	Q16042	Q16042 homo sapien	
2	291.5	25.7	433	11	Q912M6	Q912M6 rattus norv	
3	290	25.6	459	11	Q62327	Q62327 mus musculus	
4	285.5	25.2	300	4	Q95407	Q95407 homo sapien	
5	276.5	24.4	482	11	Q88734	Q88734 mus musculus	
6	252.5	22.3	203	4	Q9BYU0	Q9BYU0 homo sapien	
7	251.5	22.2	260	11	Q99NE0	Q99NE0 mus musculus	
8	243.5	21.5	222	11	Q99NE1	Q99NE1 mus musculus	
9	243.5	21.5	234	11	Q99NE2	Q99NE2 mus musculus	
10	242.5	21.4	283	6	Q9XS28	Q9XS28 cercopithec	
11	242.5	21.4	401	11	Q08712	Q08712 mus musculus	
12	240	21.2	186	12	Q72735	Q72735 cowpox viru	
13	239.5	21.1	372	4	Q9UH4	Q9UH4 homo sapien	
14	239.5	21.1	401	4	Q00300	Q00300 homo sapien	
15	238	21.0	302	13	Q9PU50	Q9PU50 salvelinus	
16	235.5	20.8	401	11	Q08727	Q08727 rattus norv	

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Db 3 TCR--LREYDQTAQMCCKSPGQHAKEVCTKTSITVDCSDSDSTYTQIWNVPECLSC 60
QY 75 R---PCDPVMGLIEIAPCTSKRKTQCCQPGMFCFAWALE--CTHCELLSDCPPG-----T 125
Db 61 GSRSSDQV---ETQACTREQNRICTRCPGWYCALSKOEGCRCLCAPLRKCRPGFGVARP 116
QY 126 EAEKDEVKGNHVCPCAKGHFQNTSSPSARCPHTRCENQGLVDAAPGTAQSDTTC-- 183
Db 117 GTETSDVW-----CKCPAGPFTSNTTSDICRPHQICN---VVAIPGNASMDAVCT'S 166
QY 184 KNPLEPLPP 192
Db 167 TSPTSRWAP 175

RESULT 2
Q912M6 PRELIMINARY; PRT; 433 AA.
AC Q912M6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport
RT through the blood-brain barrier."
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 25.7%; Score 291.5; DB 11; Length 433;
Best Local Similarity 33.3%; Pred. No. 1.8e-23;
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASENQTCDQKEEYEPQHRIICSCPCPGTYVVSAKCSRIRDTVCATCAENSNEHWNY 67
Db 11 PYKPEGNQCQISQEIYDKRAQMCCKACPPGQYAKHFCNKTSITVDCADCAAGMFTQVWNH 70
QY 68 LITCQLC-RPC--DPVMGLEIAPCTSKRKTQCCQPGMFCFA--AWALECTHCELLSDCP 122
Db 71 LHTCLSCSSCSDQV----ETHNCTKKQNRVCACNADSYCALKLSHGNCRCMKLSKGG 126
QY 123 PGTEAEKDEVGKGNHVCPCAKGHFQNTSSPSARCPHTRCENQGLVDAAPGTAQSDTT 182
Db 127 PGF-GVARSRTSGNVICSACAPGTSDTTSSTDVCRPHRCS----ILAIPGNASTDAV 181
QY 183 KNPLEPLPPMSGT 197
Db 182 CASE-SPTPSAVPRT 195

RESULT 3
Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE MURINE TUMOUR NECROSIS FACTOR RECEPTOR 2 PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice."
RL Genomics 0:0-0(0).
RN 2;
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene."
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 87 87
FT VARIANT 93 93
FT VARIANT 268 268
FT VARIANT 345 345
FT VARIANT 421 421
FT VARIANT 421 421
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 25.6%; Score 290; DB 11; Length 459;
Best Local Similarity 33.5%; Pred. No. 2.8e-23;
Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASE-NQTCRDOEKEYEPOHRIICSCPCPGTYVVSAKCSRIRDTVCATCAENSNEHWN 66
Db 16 PYKPEPGVEGQISQ-EYDRAQMCCKACPPGQYVYKHFNCNKTSITVDCADCEASMTQVWN 74
QY 67 YLTICQLCR---PCDPVMGLEIAPCTSKRKTQCCQPGMFCFA--AWALECTHCELLSDC 121
Db 75 QPRTCLSCSSCSDQV----ETRACTKQNRVCACERAGRYCALKTHSSSCRCQMLSKC 130
QY 122 PGTEAEKDEVGKGNHVCPCAKGHFQNTSSPSARCPHTRCENQGLVDAAPGTAQSDT 181
Db 131 GPGE-GVASSRAPNGNLCKACAPGTSDTTSSTDVCRPHRCS----ILAIPGNASTDA 185.
QY 182 TCKNPLEPLPPMS 195
Db 186 VC---APESPTLS 195

RESULT 4
Q95407 PRELIMINARY; PRT; 300 AA.
AC Q95407;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583p15.1.1) (TUMOR NECROSIS
DE FACTOR RECEPTOR SUPERFAMILY, MEMBER 6B, DECOY).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99087326; PubMed=9872321;
```

RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel P.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
 RA Goddard A.D., Botstein D., Ashkenazi A.;
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RT colon cancer.";
 RN Nature 396:699-703(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE-BLOOD;
 RC TISSUE-PANCREAS;
 RX MEDLINE=9253915; PubMed=10318773;
 RA Yu K.Y., Kwon B., Mi J., Zhai Y., Ebner R., Kwon B.S.;
 RA "A newly identified member of tumor necrosis factor receptor
 RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
 RL J. Biol. Chem. 274:13733-13736(1999).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE-PANCREAS;
 RX MEDLINE=20122600; PubMed=10655513;
 RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 RT "Overexpression of M68/DcR3 in human gastrointestinal tract tumors
 RT independent of gene amplification and its location in a four-gene
 RT cluster.";
 RL proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP Matthews L.;
 RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RC TISSUE-LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED.;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF104419; AAD03056.1; -
 DR EMBL; AF134240; AAD29698.1; -
 DR EMBL; AF217796; AAF35244.1; -
 DR EMBL; AF217793; AAF33685.1; -
 DR EMBL; AF217794; AAF33686.1; -
 DR EMBL; AL121845; CAC03668.1; -
 DR EMBL; BC017065; AAH17065.1; -
 DR HSP; O14763; 1D0G.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 KW Receptor.
 SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;

Query Match 25.2%; Score 285.5; DB 4; Length 300;
 Best Local Similarity 36.0%; Pred. No. 5.7e-23;
 Matches 63; Conservative 18; Mismatches 77; Indels 17; Gaps 7;
 QY 25 EPOHRCRCPPGTYVSAKCSRIKRDVTCATCAENSYNEHNYLTICQLCRPCDPVWG-- 82
 DB 42 ETGERLVCAQCPPGTFVORPCRRSDSPITCGPCPPRHRYTQFWNYL---ERCYCNVLCGER 98
 QY 83 LEEIAPCTSKRKTQCRCPGMFC-AAWALECTHCELLSDCPPGTEAEKDEVGKGNHCV 141
 DB 99 EEEARACHATHNRCRCCTGFFAAGFCLC---H---ASCPPGA-GVIAPCTPSQNTCCQ 151
 QY 142 PCKAGHFONTSSPARGCPHTRCNQGLVEAPGTAOSDTCKN-----PLEPLPP 192
 DB 152 PCPPGTFSSSSSEQCPHRCNCTALGLALNVPGSSSHDTLTCTGTFPLSTRVP 206

RESULT 5
 O88734

ID O88734 PRELIMINARY; PRT; 482 AA.
 AC O88734;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P80 TNF-ALPHA RECEPTOR.
 DE TNFR2.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98414512; PubMed=9740674;
 RX Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
 RA "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
 RT and Characterization of the two Transcripts.";
 RL Genomics 52:79-98(1998).
 DR EMBL; Y14619; CAA74969.1; -
 DR EMBL; Y14620; CAA74969.1; JOINED.
 DR EMBL; Y14621; CAA74969.1; JOINED.
 DR EMBL; Y14622; CAA74969.1; JOINED.
 DR EMBL; Y14623; CAA74969.1; JOINED.
 DR EMBL; Y14623; CAA74969.1; JOINED.
 DR HSP; P19438; INCF.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 KW Receptor.
 SQ SEQUENCE 482 AA; 51106 MW; F6C1504648FF83C CRC64;
 Query Match 24.4%; Score 276.5; DB 11; Length 482;
 Best Local Similarity 32.3%; Pred. No. 8.5e-22;
 Matches 65; Conservative 24; Mismatches 85; Indels 27; Gaps 9;
 QY 8 PYASE-NQTCRQDEKEYEYEQHRCSCSPGTYVSAKCSRI-----RDTVCATCAEN 59
 DB 31 PYKEPGVEQISQ-EYDRAQMCCKAPGQVVKHFCNKTSDTVCAADSDTVCADEAS 89
 QY 60 SYNEHNYLTICQLCR---PCDPVWGLEEIIAPCTSKRKTQCRCPGMFC--AWALECTH 114
 DB 90 MYTQWVNFRTCLSCSSSCSTDQV----ETRACTQQRNVCAACEAGRYCALKTHSGSCRQ 145
 QY 115 CELSDCPPGTEAEKDEVGKGNHCVCKAGHFNQNTSSPARGCPHTRCNQGLVEAP 174
 DB 146 CMRLSKCGPGF-GVASSRAPNGNYLCKACAPGTSTSTSDTVCKPHRCS-----ILAIP 200
 QY 175 GTAOSDTCKNPLEPLPPMS 195
 DB 201 GNASTDVAVC-----APESEPTLS 217
 RESULT 6
 QYBYUO PRELIMINARY; PRT; 203 AA.
 ID QYBYUO
 AC QYBYUO
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CD40 TYPE II ISOFORM.
 GN CD40.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21117110; PubMed=11172023;
 RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;

RT "Regulation of CD40 function by its isoforms generated through
 RT alternative splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

DR EMBL: AJ300189; CAC29424.1; -
 DR HSSP: P25942; 1CDF.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 3.
 DR ProDom: PD000711; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 DR PROSITE: PS00050; TNFR_NGFR_2; 3.
 SQ SEQUENCE 203 AA; 22259 MW; 07399D5F79D59A4F CRC64;

Query Match 22.3%; Score 252.5; DB 4; Length 203;
 Best Local Similarity 33.2%; Pred. No. 1.5e-19;
 Matches 63; Conservative 21; Mismatches 75; Indels 31; Gaps 8;

QY 7 PYASENOTCQDEKEYEYPOHRIICCSRCPPGTYVSAKCSRIKRDVTCATCAENSYNHWN 66
 DB 22 PPTA-----CR-EKQYLNSQ--CCSLCOPGQKLVSDCTETETECPLCGESEFLDTWN 72
 QY 67 YITICQLCRPCDPVGMGLEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPPGTE 126
 DB 73 RETHCHQHYCDPNLGLRVQKGTSETDICTCEBWHCTSEA--CESVLHRSCTSPGFG 130
 QY 127 AELKDEVGKGNHCVPCAKGHFQNTSSPSARCOPHTRCENQGLVEAAGTAAQS----- 179
 DB 131 VK-QIATGVSDTICEPCPVGVFFSNVSSAFKCHPWTR-----SPGSAESPGGDPHH 180
 QY 180 --DTTCKNPL 187
 DB 181 LRDPVC-HPL 189

RESULT 7
 Q99NEO PRELIMINARY; PRT; 260 AA.
 AC Q99NEO;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CD40 TYPE V ISOFORM.
 GN CD40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21117110; PubMed=11172023;
 RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
 RT "Regulation of CD40 function by its isoforms generated through
 RT alternative splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
 DR EMBL: AJ401390; CAC29430.1; -
 DR HSSP: P25942; 1CDF.
 DR InterPro: IPR001005; Myb_DNA_bind.
 DR InterPro: IPR001865; Ribosomal_S2.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom: PD000711; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 4.
 SQ SEQUENCE 260 AA; 28895 MW; 57A5BAC8CF2F546 CRC64;

Query Match 22.2%; Score 251.5; DB 11; Length 260;

Best Local Similarity 31.7%; Pred. No. 2.4e-19;
 Matches 60; Conservative 22; Mismatches 84; Indels 23; Gaps 7;
 QY 15 TCRDQKEYEYPOHRIICCSRCPPGTYVSAKCSRIKRDVTCATCAENSYNHWNLYTICQLC 74
 DB 25 TCSD--KOYLHDGQ--CCDLCOPGSRLLTSHCTALEKTQCHPCDSEGEFSAQNMREIRCHQH 80
 QY 75 RCPDPMGLEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPPG-----TEAEL 129
 DB 81 RHCEPNOGLRVKKEGTAEVDVTCCKEGQHCT--SKDCEACAOHTPCIPGFGVEMMATET 138
 QY 130 KDEYKGNHCVPCAKGHFQNTSSPSARCOPHTRCENQGLVEAAGTAAQSOTTC-----KN 185
 DB 139 TDTV-----CHPCPVGVFFSNQSSLFKCYPWTSCEDKNLEVLQKGTSGTNTVICKVVKK 192
 QY 186 PL--EPLPP 192
 DB 193 PRDNEMLPP 201

RESULT 8
 Q99NE1 PRELIMINARY; PRT; 222 AA.
 AC Q99NE1;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CD40 TYPE IV ISOFORM.
 GN CD40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21117110; PubMed=11172023;
 RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
 RT "Regulation of CD40 function by its isoforms generated through
 RT alternative splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
 DR EMBL: AJ401389; CAC29429.1; -
 DR HSSP: P25942; 1CDF.
 DR InterPro: IPR001005; Myb_DNA_bind.
 DR InterPro: IPR001865; Ribosomal_S2.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom: PD000711; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 4.
 SQ SEQUENCE 222 AA; 24499 MW; EE21B6C76FB42DEF CRC64;

Query Match 21.5%; Score 243.5; DB 11; Length 222;
 Best Local Similarity 31.0%; Pred. No. 1.5e-18;
 Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;
 QY 15 TCRDQKEYEYPOHRIICCSRCPPGTYVSAKCSRIKRDVTCATCAENSYNHWNLYTICQLC 74
 DB 25 TCSD--KOYLHDGQ--CCDLCOPGSRLLTSHCTALEKTQCHPCDSEGEFSAQNMREIRCHQH 80
 QY 75 RCPDPMGLEIACTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPPG-----TEAEL 129
 DB 81 RHCEPNOGLRVKKEGTAEVDVTCCKEGQHCT--SKDCEACAOHTPCIPGFGVEMMATET 138
 QY 130 KDEYKGNHCVPCAKGHFQNTSSPSARCOPHTRCENQGLVEAAGTAAQSOTTC 183
 DB 139 TDTV-----CHPCPVGVFFSNQSSLFKCYPWTSCEDKNLEVLQKGTSGTNTVICK 186

RESULT 9

Q99NE2	Q99NE2	PRELIMINARY;	PRT;	234 AA.
ID	Q99NE2			
AC	Q99NE2;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	CD40 TYPE III ISOFORM.			
GN	CD40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
SEQUENCE	FROM N.A.			
RL	MEDLINE=21117110; PubMed=11172023;			
RX	Tone M., Tone Y., Fairchild P.J., Wykes M., Waidmann H.;			
RT	"Regulation of CD40 function by its isoforms generated through			
RT	alternative splicing";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).			
DR	EMBL; AJ401388; CAC29428.1; -.			
DR	HSSP; P25942; 1CDF.			
DR	InterPro; IPR001005; MYB_DNA_bind.			
DR	InterPro; IPR001865; Ribosomal_S2.			
DR	InterPro; IPR001368; TNFR_c6.			
DR	Pfam; PF00020; TNFR_c6; 4.			
DR	PRODOM; PD000771; TNFR_c6; 1.			
DR	SMART; SM00208; TNFR; 4.			
DR	PROSITE; PS00037; MYB_1; UNKNOWN_1.			
DR	PROSITE; PS00062; RIBOSOMAL_S2_1; UNKNOWN_1.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 4.			
SQ	SEQUENCE 234 AA; 25747 MW; 00DB1DD38347E325 CRC64;			
Query Match	21.5%;	Score 243.5;	DB 11;	Length 234;
Best Local Similarity	31.0%;	Pred. No. 1.6e-18;		
Matches	54; Conservative	22; Mismatches	81; Indels	17; Gaps
QY	15	TCRQEEYEPQHRICCSRCPPGTGVYSAKCSIRDTVCATCAENSYNHWNLYLTICQLC 74		
DB	25	TCSD--KQYLDHGQ--CCDLCPGSRLTSHCTALEXTQCHPCDSGEFSAQWNRIRCHQH 80		
QY	75	RPDVPVNGLBELAPCTSKRTQCRQOPGMFCAAWALECTHCELLSDCPG-----TEAL 129		
DB	81	RHCEPNGLRVKKEGTAESTDVTCKEGQHT--SKDCEACAGHTPCIPFGVGMEMATET 138		
QY	130	KDEVGKNNHCVCCKAGHFONTSPSARCOPHTRCENOGIVEAPGTASDTTC 183		
DB	139	TDTV-----CHPCPVGVFFSNQSLFEKCYPTWSCDKNLEVLRKGTSTQNVIC 186		
RESULT	10			
Q9XSZ8	Q9XSZ8	PRELIMINARY;	PRT;	283 AA.
ID	Q9XSZ8			
AC	Q9XSZ8;			
DT	01-NOV-1999 (TrEMBLrel. 12, Created)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	HVEAS.			
GN	HVEAS.			
OS	Cercopithecus aethiops (Green monkey) (Grivet).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OX	Cercopithecinae; Cercopithecus.			
OX	NCBI_TaxID=9534;			
RN	[1]			
SEQUENCE	FROM N.A.			
RP	TISSUE=KIDNEY;			
RC	MEDLINE=99296730; PubMed=10366573;			
RX	Foster T.P., Chouljenko V.N., Kousoulas K.G.;			
RA	"Functional characterization of the HveA homolog specified by African			
RT	green monkey kidney cells with a herpes simplex virus expressing the			
RT	green fluorescence protein.;"			

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Virology 258:365-374(1999).
DR EMBL; AF147720; AAD37381.1; -.
DR HSPSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

Query Match          21.4%; Score 242.5; DB 6; Length 283;
Best Local Similarity 32.2%; Pred. No. 2.4e-18;
Matches 57; Conservative 18; Mismatches 85; Indels 17; Gaps

Qy      9 YASENOTCRDOEKVEYEPQHRIICSCRCPPCTGYVSAKCSRIIRDVTVCATCAENSNEHNYVL 68
       || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     35 YAPALPSCK--EDBY--PVSECCPKCGPFHVQRACGEQTGVCPKSPCYIAHFNGL 90
       :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy     69 TICOLCRPCDPVMGLEEIAPTCKRRKTQCRCQPMFCAAW-ALECHTHCELLSDCPPGTEA 127
       :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    91 SKCLQCQMCDFAMGLRTSRNCSTTANALGCSPGHFCIIQGDHCAACRAYATSSPG--- 147
       :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   128 ELKDVEKGNNH-----CVPCKAGHFONTSSPARGCPHTRCENQGLVFNAEPAQTAS 179
       |||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   148 --ORVKGGTGESODTLTCQNCPPGTF--SSNGTLEECHGNKCCKLVLTAEAGPGTSSS 200
       :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 11
O08712 PRELIMINARY; PRT; 401 AA.
AC O08712; 070202;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
DE OSTEOPODTERGIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF).
GN TNFRSF11B OR OPG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=KIDNEY;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Jacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/OLA, AND NIH SWISS;
RX MEDLINE=96382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
gene and its expression in embryogenesis.";
RL Gene 215:339-345(1998).
CC -! FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC ° STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -! SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
CC -! SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -! TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
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DR Pfam; PF00020; TNFR_c6; 3.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 FT NON_TER 1
 SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 21.1%; Score 239.5; DB 4; Length 372;
 Best Local Similarity 30.9%; Pred. No. 6.8e-18;
 Matches 51; Conservative 21; Mismatches 84; Indels 9; Gaps 4;

Qy 25 EPQHRICSRCPGGTYVSAGKSRIRDTVCATCAENSYNEHWNLYLTICOLCRP-CDPVNGL 83
 Db 13 ETSHQLLCKCPGGTYLQKHCTAKWKTCAPCPDHYTDSWHTSDECLYCSPVKELQYV 72
 Qy 84 EBIAPCTSKRTQCRQCPGMCFAWALECTHCELLSDCPPGTEAEKDEKGVGNHCVPC 143
 Db 73 KO--ECNRTHNRVCEKEGRY-----LETEFLKHRSCPPGF-GVVQAGTPERNTVCKRC 124
 Qy 144 KAGHFQNTSSPSARCPHTRCENOGVLEAAPTQAQSDTTCKNPLE 188
 Db 125 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNCISGENSE 169

RESULT 14
 O00300 PRELIMINARY; PRT; 401 AA.

ID O00300; O60236;
 AC O00300; O60236;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
 GN TNFRSF11B OR OPG OR OCIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Sugds S., Boyle W.J.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density";
 RL Cell 89:309-319(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG FIBROBLAST;
 RX MEDLINE=98151033; PubMed=9492069;
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 RA Sato Y., Goto M., Yamauchi K., Kuriyama M., Kanno T., Murakami A.,
 RA Tsuda E., Morinaga T., Higashio K.;
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 RT osteoclastogenesis in vitro";
 RL Endocrinology 139:1329-1337(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RX MEDLINE=98351569; PubMed=9688283;
 RA Morinaga T., Nakagawa N., Yasuda E., Tsuda E., Higashio K.;
 RT "Cloning and characterization of the gene encoding human
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor";
 RL Eur. J. Biochem. 254:685-691(1998).

CC Pfam; PF00020; TNFR_c6; 3.
 CC ProDom; PD000771; TNFR_c6; 1.
 CC SMART; SM00005; DEATH; 1.
 CC SMART; SM00208; TNFR; 4.
 CC PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 CC PROSITE; PS00650; TNFR_NGFR_2; 2.
 CC NON_TER 1
 CC SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 21.1%; Score 239.5; DB 4; Length 401;
 Best Local Similarity 30.9%; Pred. No. 7.3e-18;
 Matches 51; Conservative 21; Mismatches 84; Indels 9; Gaps 4;

Qy 25 EPQHRICSRCPGGTYVSAGKSRIRDTVCATCAENSYNEHWNLYLTICOLCRP-CDPVNGL 83
 Db 34 ETSHQLLCKCPGGTYLQKHCTAKWKTCAPCPDHYTDSWHTSDECLYCSPVKELQYV 93
 Qy 84 EBIAPCTSKRTQCRQCPGMCFAWALECTHCELLSDCPPGTEAEKDEKGVGNHCVPC 143
 Db 94 KO--ECNRTHNRVCEKEGRY-----LETEFLKHRSCPPGF-GVVQAGTPERNTVCKRC 145
 Qy 144 KAGHFQNTSSPSARCPHTRCENOGVLEAAPTQAQSDTTCKNPLE 188
 Db 146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNCISGENSE 190

RESULT 15
 Q9PUS0 PRELIMINARY; PRT; 302 AA.
 ID Q9PUS0
 AC Q9PUS0;

